HLA BINDING PEPTIDES AND THEIR USES

Field of the Invention

The invention relates to peptides that bind major histocompatibility (MHC) molecules and the use of these peptides to induce and modulate an immune response.

Background

The recognition of foreign pathogens, foreign cells (*e.g.*, tumor), or one's own cells by the immune system occurs largely through major histocompatibility (MHC) molecules. MHC molecules present unique molecular fragments of foreign and self molecules that permit recognition and, when appropriate, stimulation of various immune effectors, namely B and T lymphocytes. MHC molecules are classified as either class I or class II. Class II MHC molecules are expressed primarily on activated lymphocytes and antigen-presenting cells. CD4+ T lymphocytes are activated with recognition of a unique peptide fragment presented by a class II MHC molecule, usually found on an antigen presenting cell like a macrophage or dendritic cell. Often known as helper T lymphocytes (HTL), CD4+ lymphocytes proliferate and secrete cytokines that either support a antibody-mediated response through the production of IL-4 and IL-10 or support a cell-mediated response through the production of IL-2 and IFN-γ. Class I MHC molecules, on the other hand, are expressed on virtually all nucleated cells. Peptide fragments presented in the context of Class I MHC molecules are recognized by CD8+ T lymphocytes. CD8+ T lymphocytes frequently mature into cytotoxic effector which can lyse cells bearing the stimulating antigen. Otherwise known as cytotoxic T lymphocytes (CTLs), CTLs are particularly effective in eliminating tumor cells and in fighting viral infections.

T lymphocytes recognize an antigen in the form of a peptide fragment bound to the MHC class I or class II molecule rather than the intact foreign antigen itself. An antigen presented by a MHC class I molecule is typically one that is endogenously synthesized by the cell (*e.g.*, an intracellular pathogen). The resulting cytoplasmic antigens are degraded into small

fragments in the cytoplasm, usually by the proteosome (Niedermann *et al.*, *Immunity*, 2: 289-99(1995)). Some of these small fragments are transported into the endoplasmic reticulum where the fragment interacts with class I heavy chains to facilitate proper folding and association with the subunit β2 microglobulin to result in a stable complex formation between the fragment, MHC class I chain and β2 microglobulin. This complex is then transported to the cell surface for expression and potential recognition by specific CTLs. Antigens presented by MHC class II molecules are usually soluble antigens that enter the antigen presenting cell via phagocytosis, pinocytosis, or receptor-mediated endocytosis. Once in the cell, the antigen is partially degraded by acid-dependent proteases in endosomes. The resulting fragments or peptide associate with the MHC class II molecule after the release of the CLIP fragment to form a stable complex that is then transported to the surface for potential recognition by specific HTLs. *See* Blum *et al.*, *Crit. Rev. Immunol.*, 17: 411-17 (1997); Arndt *et al.*, *Immuno.l Res.*, 16: 261-72 (1997).

Peptides that bind some MHC complexes have been identified by acid elution methods (Buus *et al.*, *Science* 242: 1065 (1988)), chromatography methods (Jardetzky, *et al.*, *Nature* 353: 326 (1991) and Falk *et al.*, *Nature* 351: 290 (1991)), and by mass spectrometry methods (Hunt, *et al.*, *Science* 225: 1261 (1992)). A review of naturally processed peptides that bind MHC class I molecules is set forth in Rötzschke and Falk, *Immunol. Today* 12: 447 (1991).

Peptides that bind a particular MHC allele frequently will fit within a motif and have amino acid residues with particular biochemical properties at specific positions within the peptide. Such residues are usually dictated by the biochemical properties of the MHC allele. Peptide sequence motifs have been utilized to screen peptides capable of binding MHC molecules (Sette *et al.*, *Proc. Natl. Acad. Sci. USA* 86:3296 (1989)), and it has been reported that class I binding motifs identified potential immunogenic peptides in animal models (De Bruijn *et al.*, *Eur. J. Immunol. 21*: 2963-2970 (1991); Pamer *et al.*, *Nature 353*: 852-955 (1991)). Also, binding of a particular peptide to a MHC molecule has been correlated with immunogenicity of that peptide (Schaeffer *et al.*, *Proc. Natl. Acad. Sci. USA* 86:4649 (1989)).

Of the many thousand possible peptides that are encoded by a complex foreign pathogen, only a small fraction ends up in a peptide form capable of binding to MHC class I or class II antigens and thus of being recognized by T cells. This phenomenon is known as immunodominance (Yewdell *et al.*, *Ann. Rev. Immunol.*, 17: 51-88 (1997)). More simply, immunodominance describes the phenomenon whereby immunization or exposure to a whole native antigen results in an immune response directed to one or a few "dominant" epitopes of the antigen rather than every epitope that the native antigen contains. Immunodominance is influenced by a variety of factors that include MHC-peptide affinity, antigen processing, and antigen availability.

Accordingly, while some MHC binding peptides have been identified, there is a need in the art to identify novel MHC binding peptides from pathogens that can be utilized to generate an immune response in vaccines against the pathogens from which they originate. Further, there is a need in the art to identify peptides capable of binding a wide array of different types of MHC molecules such they are immunogenic in a large fraction a human outbred population.

Summary

The present invention relates to compositions and methods for preventing, treating or diagnosing a number of pathological states such as viral diseases and cancers. Thus, provided herein are novel peptides capable of binding selected major histocompatibility complex (MHC) molecules and inducing or modulating an immune response. Some of the peptides disclosed are capable of binding human class II MHC (HLA) molecules, including HLA-DR and HLA-DQ alleles. Other peptides disclosed herein are capable of binding to human class I molecules, including one or more of the following: HLA-A1, HLA-A2.1, HLA-A3.2, HLA-A11, HLA-A24.1, HLA-B7, and HLA-B44 molecules. Other peptides disclosed are capable of binding to murine class I molecules. Also provided are compositions that include immunogenic peptides having binding motifs specific for MHC molecules. The peptides and compositions disclosed can be utilized in methods for inducing an immune response, a cytotoxic T lymphocyte (CTL) response or helper T lymphocyte (HTL) response in particular, when administered to a

system. The peptides and compositions disclosed herein are also useful as diagnostic reagents (*e.g.*, tetramer reagents; Beckman Coulter).

Brief Description of the Drawings

Figure 1. Preferred Motif Table.

Figure 2. HLA superfamilies for HLA-A and HLA-B alleles. Various alleles of HLA-A and HLA-B are classified according to superfamily based on sequencing analysis or binding assays (verified supertype members) or on the basis of B and F pocket structure (predicted supertype members).

Definitions

The following definitions are provided to enable one of ordinary skill in the art to understand some of the preferred embodiments of invention disclosed herein. It is understood, however, that these definitions are exemplary only and should not be used to limit the scope of the invention as set forth in the claims. Those of ordinary skill in the art will be able to construct slight modifications to the definitions below and utilize such modified definitions to understand and practice the invention disclosed herein. Such modifications, which would be obvious to one of ordinary skill in the art, as they may be applicable to the claims set forth below, are considered to be within the scope of the present invention. If a definition set forth in this section is contrary to or otherwise inconsistent with a definition set forth in patents, published patent applications and other publications and sequences from GenBank and other data bases that are herein incorporated by reference, the definition set forth in this section prevails over the definition that is incorporated herein by reference.

As used herein, the term "HLA supertype or HLA family," refers to sets of HLA molecules grouped based on shared peptide-binding specificities. The terms HLA superfamily, HLA supertype family, HLA family, and HLA xx-like molecules (where xx denotes a particular HLA type), are synonyms.

As used herein, the term "IC_{50}" refers to the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Depending on the conditions in which the assays are run (*e.g.*,

limiting MHC proteins and labeled peptide concentrations), these values may approximate K_D values.

As used herein, the term "peptide" is used interchangeably with "epitope" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the α-amino and carboxyl groups of adjacent amino acids, that binds to a designated MHC allele.

As used herein, the term "pharmaceutically acceptable" refers to a generally non-toxic, inert, and/or physiologically compatible composition.

As used herein, the term "protective immune response" or "therapeutic immune response" refers to a CTL and/or an HTL response to an antigen derived from an infectious agent or a tumor antigen, which in some way prevents or at least partially arrests disease symptoms, side effects or progression. The immune response may also include an antibody response that has been facilitated by the stimulation of helper T cells.

As used herein, the term "residue" refers to an amino acid or amino acid mimetic incorporated in a peptide by an amide bond or amide bond mimetic.

As used herein, the term "motif" refers to the pattern of residues in a peptide of defined length, usually a peptide of from about 8 to about 13 amino acids for a class I MHC motif and from about 6 to about 25 amino acids for a class II MHC motif, which is recognized by a particular MHC molecule. Peptide motifs are typically different for each protein encoded by each MHC allele and differ in the pattern of the highly conserved and negative residues.

As used herein, the term "supermotif" refers to an amino acid sequence for a peptide that provides binding specificity shared by MHC molecules encoded by two or more MHC alleles. Preferably, a supermotif-bearing peptide is recognized with high or intermediate affinity (as defined herein) by two or more MHC antigens.

As used herein, the term "conserved residue" refers to an amino acid which occurs in a significantly higher frequency than would be expected by random distribution at a particular position in a peptide. Typically a conserved residue is one where the MHC structure may provide a contact

point with the immunogenic peptide. At least one to three or more, preferably two, conserved residues within a peptide of defined length defines a motif for an immunogenic peptide. These residues are typically in close contact with the peptide binding groove, with their side chains buried in specific pockets of the groove itself. Typically, an immunogenic peptide will comprise up to three conserved residues, more usually two conserved residues.

As used herein, "negative binding residues" are amino acids which if present at certain positions (for example, positions 1, 3, 6 and/or 7 of a 9-mer) will result in a peptide being a nonbinder or poor binder and in turn fail to be immunogenic, *e.g.*, induce a CTL response.

As used herein, the term "synthetic peptide" refers to a peptide that is not naturally occurring, but is man-made using such methods as chemical synthesis or recombinant DNA technology.

As used herein, the term "immunogenic peptide" refers to a peptide which comprises an allele-specific motif such that the peptide will bind an MHC molecule and induce a CTL or HTL response. An immunogenic response includes one that stimulates a CTL and/or HTL response *in vitro* and/or *in vivo* as well as modulates an ongoing immune response through directed induction of cell death (or apoptosis) in specific T cell populations.

As used herein, the phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany it as found in its native state. Thus, the peptides of this invention do not contain materials normally associated with their in situ environment, *e.g.*, MHC I molecules on antigen presenting cells. Even where a protein has been isolated to a homogeneous or dominant band, there are trace contaminants in the range of 5-10% of native protein which co-purify with the desired protein. Isolated peptides of this invention do not contain such endogenous co-purified protein.

Nomenclature used to describe peptide compounds follows the conventional practice wherein the amino group is presented to the left (the N-terminus) and the carboxyl group to the right (the C-terminus) of each amino acid residue. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH

values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G.

Detailed Description

A. Peptide and Motif Identification

The present invention relates to allele-specific peptide motifs and binding peptides for human and murine MHC allele. It is contemplated that the peptide binding motifs of the invention are relatively specific for each allele. In an embodiment of the invention, the allele-specific motifs and binding peptides are for human class I MHC (or HLA) alleles. HLA alleles include HLA-A, HLA-B, and HLA-C alleles. In another embodiment of the invention the allele-specific motifs and binding peptides are for human class II MHC (or HLA) alleles. Such HLA alleles include HLA-DR and HLA-DQ alleles. HLA molecules that share similar binding affinity for peptides bearing certain amino acid motifs are grouped into HLA supertypes. *See, e.g.*, Stites, *et al.*, IMMUNOLOGY, 8TH ED., Lange Publishing, Los Altos, CA (1994). Peptides that bind one or more alleles in one or more supertypes are contemplated as part of the invention. Examples of the supertypes within HLA-A and HLA-B molecules are shown in Figure 2. In yet another embodiment, the allele-specific motifs and binding peptides are for murine class I (or H-2) MHC alleles. Such H-2 alleles include H-2Dd, H-2Kb, H-2Kd, H-2Db, H-2Ld, and H-2Kk. Exemplary tables describing allele-specific motifs are presented below. Binding within a particular supertype for murine MHC alleles is also contemplated.

To identify peptides of the invention, MHC-peptide complex isolation, and isolation and sequencing of naturally processed peptides was carried out as described in the related applications. This application may be relevant to U.S.S.N. 09/189,702 filed 11/10/98, which is a CIP of U.S.S.N 08/205,713

filed 3/4/94, which is a CIP of 08/159,184 filed 11/29/93 and now abandoned, which is a CIP of 08/073,205 filed 6/4/93 and now abandoned, which is a CIP of 08/027,146 filed 3/5/93 and now abandoned. The present application is also related to U.S.S.N. 09/226,775, which is a CIP of U.S.S.N. 08/815,396, which claims the benefit of U.S.S.N. 60/013,113, now abandoned. Furthermore, the present application is related to U.S.S.N. 09/017,735, which is a CIP of abandoned U.S.S.N. 08/589,108; U.S.S.N. 08/753,622, U.S.S.N. 08/822,382, abandoned U.S.S.N. 60/013,980, U.S.S.N. 08/454,033, U.S.S.N. 09/116,424, and U.S.S.N. 08/349,177. The present application is also related to U.S.S.N. 09/017,524, U.S.S.N. 08/821,739, abandoned U.S.S.N. 60/013,833, U.S.S.N. 08/758,409, U.S.S.N. 08/589,107, U.S.S.N. 08/451,913, U.S.S.N. 08/186,266, U.S.S.N. 09/116,061, and U.S.S.N. 08/347,610, which is a CIP of U.S.S.N. 08/159,339, which is a CIP of abandoned U.S.S.N. 08/103,396, which is a CIP of abandoned U.S.S.N. 08/027,746, which is a CIP of abandoned U.S.S.N. 07/926,666. The present application may also be relevant to U.S.S.N. 09/017,743, U.S.S.N. 08/753,615; U.S.S.N. 08/590,298, U.S.S.N. 09/115,400, and U.S.S.N. 08/452,843, which is a CIP of U.S.S.N. 08/344,824, which is a CIP of abandoned U.S.S.N. 08/278,634. The present application may also be related to provisional U.S.S.N. 60/087,192 and U.S.S.N. 09/009,953, which is a CIP of abandoned U.S.S.N. 60/036,713 and abandoned U.S.S.N. 60/037,432. In addition, the present application may be relevant to U.S.S.N. 09/098,584, and U.S.S.N. 09/239,043. The present application may also be relevant to co-pending U.S.S.N. 09/583,200 filed 5/30/00, U.S.S.N. 09/260,714 filed 3/1/99, and U.S. Provisional Application "Heteroclitic Analogs And Related Methods", Attorney Docket Number 018623-015810US filed 10/6/00 . All of the above applications are incorporated herein by reference.

These peptides were then used to define specific binding motifs for each of the following alleles A3.2, A1, A11, and A24.1. These motifs are described previously. The motifs described in Tables 1-4, below, are defined from pool sequencing data of naturally processed peptides as described in the related applications. Preferred (*i.e.*, canonical) and tolerated (*i.e.*, extended) residues associated with anchor positions of the indicated HLA supertypes are presented in Figure 1 and Table 5.

In one embodiment, the motif for HLA-A3.2 comprises from the N-terminus to C-terminus a first conserved residue of L, M, I, V, S, A, T and F at position 2 and a second conserved residue of K, R or Y at the C-terminal end. Other first conserved residues are C, G or D and alternatively E. Other second conserved residues are H or F. The first and second conserved residues are preferably separated by 6 to 7 residues. In another embodiment, the motif for HLA-A1 comprises from the N-terminus to the C-terminus a first conserved residue of T, S or M, a second conserved residue of D or E, and a third conserved residue of Y. Other second conserved residues are A, S or T. The first and second conserved residues are adjacent and are preferably separated from the third conserved residue by 6 to 7 residues. A second motif consists of a first conserved residue of E or D and a second conserved residue of Y where the first and second conserved residues are separated by 5 to 6 residues.

In yet another embodiment, the motif for HLA-A11 comprises from the N-terminus to the C-terminus a first conserved residue of T, V, M, L, I, S, A, G, N, C D, or F at position 2 and a C-terminal conserved residue of K, R, Y or H. The first and second conserved residues are preferably separated by 6 or 7 residues. In one embodiment, the motif for HLA-A24.1 comprises from the N-terminus to the C-terminus a first conserved residue of Y, F or W at position 2 and a C terminal conserved residue of F, I, W, M or L. The first and second conserved residues are preferably separated by 6 to 7 residues.

TABLE 1

Summary

HLA-A3,2 Allele-Specific Motif

Position	Conserved Residues
1	-
2	V,L,M
3	Y,D
4	-
5	-
6	-
7	I
8	Q,N
9	K
10	K

TABLE 2

Summary

HLA-A1 Allele-Specific Motif

Position	Conserved Residues
1	-
2	S,T
3	D,E
4	P
5	-
6	-
7	L
8	-
9	Y
10	K

TABLE 3

Summary

HLA-A11 Allele-Specific Motif

Position	Conserved Residues
1	-
2	T,V
3	M,F
4	-
5	-
6	-
7	-
8	Q
9	K
10	K

TABLE 4

Summary

HLA-A24.1 Allele-Specific Motif

Position	Conserved Residues
1	-
2	Y
3	I,M
4	D,E,G,K,P
5	L,M,N
6	V
7	N,V
8	A,E,K,Q,S
9	F,L
10	F,A

The MHC-binding peptides identified herein represent epitopes of a native antigen. With regard to a particular amino acid sequence, an epitope is a set of amino acid residues which is recognized by a particular antibody or T

cell receptor. Such epitopes are usually presented to lymphocytes via the MHC-peptide complex. An epitope retains the collective features of a molecule, such as primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an antibody, T cell receptor or MHC molecule. It is to be appreciated, however, that isolated or purified protein or peptide molecules larger than and comprising an epitope of the invention are still within the bounds of the invention. Moreover, it is contemplated that synthesized peptides can incorporate various biochemical changes that enhance their immunological effectiveness.

The epitopes present in the invention can be dominant, sub-dominant, or cryptic. A dominant epitope is an epitope that induces an immune response upon immunization with a whole native antigen. *See, e.g.*, Sercarz, *et al.*, *Ann.. Rev. Immunol.* 11: 729-766 (1993). Such a peptide is considered immunogenic because it elicits a response against the whole antigen. A subdominant epitope, on the other hand, is one that evokes little or no response upon immunization with whole antigen that contains the epitope, but for which a response can be obtained by immunization with an isolated epitope. Immunization with a sub-dominant epitope will prime for a secondary response to the intact native antigen. A cryptic epitope elicits a response by immunization with an isolated peptide, but fails to prime a secondary response to a subsequent challenge with whole antigen.

An epitope present in the invention can be cross-reactive or non-cross-reactive in its interactions with MHC alleles and alleles subtypes. Cross-reactive binding of an epitope (or peptide) permits an epitope to be bound by more than one HLA molecule. Such cross-reactivity is also known as degenerate binding. A non-cross-reactive epitope would be restricted to binding a particular MHC allele or allele subtype.

The epitopes of the present invention can be any suitable length. Class I molecule binding peptides typically are about 8 to 13 amino acids in length, and often 9, 10, 11, or 12 amino acids in length. These peptides include conserved amino acids at certain positions such as the second position from the N-terminus and the C-terminal position. Also, the peptides often do not include amino acids at certain positions that negatively affect binding of the peptide to the HLA molecules. For example, the peptides often do not include

amino acids at positions 1, 3, 6 and/or 7 for peptides 9 amino acid peptides in length or positions 1, 3, 4, 5, 7, 8 and/or 9 for peptides 10 amino acids in length. Further, defined herein are positions within a peptide sequence that can be utilized as criteria for selecting HLA-binding peptide. These defined positions are often referred to herein as a binding "motif."

Definition of motifs specific for different MHC alleles allows the identification of potential peptide epitopes from an antigenic protein whose amino acid sequence is known. Typically, identification of potential peptide epitopes is initially carried out using a computer to scan the amino acid sequence of a desired antigen for the presence of motifs. The epitopic sequences are then synthesized.

In general, class I peptide binding motifs generally include a first conserved residue at position two from the N-terminus (wherein the N-terminal residue is position one) and a second conserved residue at the C-terminal position (often position 9 or 10). As a specific example, the HLA A*0201 class I peptide binding motifs include a first conserved residue at position two from the N-terminus (wherein the N-terminal residue is position one) selected from the group consisting of I, V, A and T and a second conserved residue at the C-terminal position selected from the group consisting of V, L, I, A and M. Alternatively, the peptide may have a first conserved residue at the second position from the N-terminus (wherein the N-terminal residue is position one) selected from the group consisting of L, M, I, V, A and T; and a second conserved residue at the C-terminal position selected from the group consisting of A and M. If the peptide has 10 residues it will contain a first conserved residue at the second position from the N-terminus (wherein the N-terminal residue is position one) selected from the group consisting of L, M, I, V, A, and T; and a second conserved residue at the C-terminal position selected from the group consisting of V, I, L, A and M; wherein the first and second conserved residues are separated by 7 residues.

One embodiment of an HTL-inducing peptide is less than about 50 residues in length and usually consist of between about 6 and about 30 residues, more usually between about 12 and 25, and often between about 15 and 20 residues, for example 15, 16, 17, 18, 19, or 20 residues. One embodiment of an CTL-inducing peptide is 13 residues or less in length and

usually consists of about 8, 9, 10 or 11 residues, preferably 9 or 10 residues. In one embodiment, HLA-DR3 a binding is characterized by an L, I, V, M, F or Y residue at position 1 and a D or E residue at position 4. In another embodiment, HLA-DR3 b binding is characterized by an L, I, V, M, F, Y or A residue at position 1, a D, E, N, Q, S or T residue at position 4, and a K, R or H residue at position 6. In another embodiment, key anchor residues of a DR supertype binding motif are an L, I, V, M, F, W or Y residue at position 1 and an L, I, V, M, S, T, P, C or A residue at position 6. See table 5.

TABLE 5

HLA-DR motifs

	Anchor residues of HLA-DR core motifs		
	p1	p4	p6
DR supertype	LIVMFWY	--	LIVMSTPCA
DR3 a	LIVMFY	DE	--
DR3 b	LIVMFYA	DENQST	KRH

Moreover, in another embodiment, murine Db binding is characterized by an N residue at position 5 and L, I, V or M residue at the C-terminal position. In yet another embodiment, murine Kb binding is characterized by a Y or F residue at position 5 and an L, I, V or M residue at the C-terminal position. In an additional embodiment, murine Kd binding is characterized a Y or F residue at position 2 and an L, I, V, or M residue at the C-terminal position. In a further embodiment, murine Kk binding is characterized by an E or D residue at position 2 and an L, I, M, V, F, W, Y or A residue at the C-terminal position. In a further embodiment, murine Ld binding is characterized by a P residue at position 2 and an L, I, M, V, F, W or Y residue at the C-terminal position. See Table 6.

Table 6
Murine Class I Motifs

Allele	Anchor residues of mouse class I motifs			
	p2	p3	p5	C terminus
Db	--	--	N	LIVM
Dd	G	P	--	LVI
Kb	--	--	YF	LIVM
Kd	YF	--	--	LIVM
Kk	ED	--	--	LIMVA
Ld	P	--	--	LIMVFWY

The peptides present in the invention can be identified by any suitable method. For example, peptides are conveniently identified using the algorithms of the invention described in the co-pending U.S. Patent Application Serial No. 09/894,018. These algorithms are mathematical procedures that produce a score which enables the selection of immunogenic peptides. Typically one uses the algorithmic score with a binding threshold to enable selection of peptides that have a high probability of binding at a certain affinity and will in turn be immunogenic. The algorithm are based upon either the effects on MHC binding of a particular amino acid at a particular position of a peptide or the effects on binding MHC of a particular substitution in a motif containing peptide.

Peptide sequences characterized in molecular binding assays and capture assays have been and can be identified utilizing various technologies. Motif-positive sequences are identified using a customized application created at Epimmune. Sequences are also identified utilizing matrix-based algorithms, and have been used in conjunction with a "power" module that generates a predicted 50% inhibitory concentration (PIC) value. These latter methods are operational on Epimmune's HTML-based Epitope Information System (EIS) database. All of the described methods are viable options in peptide sequence selection for IC_{50} determination using binding assays.

Additional procedures useful in identifying the peptides of the present invention generally follow the methods disclosed in Falk *et al.*, *Nature*

351:290 (1991). Briefly, the methods involve large-scale isolation of MHC class I molecules, typically by immunoprecipitation or affinity chromatography, from the appropriate cell or cell line. Examples of other methods for isolation of the desired MHC molecule equally well known to the artisan include ion exchange chromatography, lectin chromatography, size exclusion, high performance liquid chromatography, and a combination of some or all of the above techniques.

For example, isolation of peptides bound to MHC class I molecules include lowering the culture temperature from 37°C to 26°C overnight to destabilize β_2 microglobulin and stripping the endogenous peptides from the cell using a mild acid treatment. The methods release previously bound peptides into the extracellular environment allowing new exogenous peptides to bind to the empty class I molecules. The cold-temperature incubation method enables exogenous peptides to bind efficiently to the MHC complex, but requires an overnight incubation at 26°C which may slow the cell's metabolic rate. It is also likely that cells not actively synthesizing MHC molecules (*e.g.*, resting PBMC) would not produce high amounts of empty surface MHC molecules by the cold temperature procedure.

Immunoprecipitation is also used to isolate the desired allele. A number of protocols can be used, depending upon the specificity of the antibodies used. For example, allele-specific mAb reagents can be used for the affinity purification of the HLA-A, HLA-B, and HLA-C molecules. Several mAb reagents for the isolation of HLA-A molecules are available (Table 5). Monoclonal antibody BB7.2 is suitable for isolating HLA-A2 molecules. Thus, for each of the targeted HLA-A alleles, reagents are available that may be used for the direct isolation of the HLA-A molecules. Affinity columns prepared with these mAbs using standard techniques are successfully used to purify the respective HLA-A allele products.

In addition to allele-specific mAbs, broadly reactive anti-HLA-A, B, C mAbs, such as W6/32 and B9.12.1, and one anti-HLA-B, C mAb, B1.23.2, could be used in alternative affinity purification protocols as described in patents and patent applications described herein.

TABLE 7

HLA CLASS I MHC MOLECULES

HLA-A,B Allele	Cell Lines	Ab utilized for Capture assay
A*0101	Steinlin, MAT	W6/32
A*2601	Pure Protein, QBL	W6/32
A*2902	Sweig, Pure Protein, Pitout	W6/32
A*3002	DUCAF, Pure Protein	W6/32
A*2301	Pure Protein, WT51	W6/32
A*2402	KT3, Pure Protein, KAS116	W6/32
A*0201	JY, OMW	W6/32
A*0202	M7B	W6/32
A*0203	FUN	W6/32
A*0205	DAH	W6/32
A*0206	CLA	W6/32
A*0207	AP	W6/32
A*6802	AMAI	W6/32
A*0301	GM3107	W6/32
A*1101	BVR	W6/32
A*3101	SPACH, OLL	W6/32
A*3301	LWAGS	W6/32
A*6801	CIR, 2F7	W6/32
B*0702	GM3107, JY	W6/32
B*3501	CIR, BVR	W6/32
B*5101	KAS116	W6/32
B*5301	AMAI	W6/32
B*5401	KT3	W6/32
B*1801	DUCAF	W6/32
B*4001	2F7	W6/32
B*4002	Sweig	W6/32
B*4402	WT47	B1.23.1
B*4403	Pitout	B1.23.1
B*4501	OMW	W6/32
A*3201	Pure Protein, WT47	W6/32

The peptides bound to the peptide binding groove of the isolated MHC molecules are typically eluted using acid treatment. Peptides can also be dissociated from MHC molecules by a variety of standard denaturing means, such as, for example, heat, pH, detergents, salts, chaotropic agents, or a combination acid treatment and/or more standard denaturing means.

Peptide fractions are further separated from the MHC molecules by reversed-phase high performance liquid chromatography (HPLC) and

sequenced. Peptides can be separated by a variety of other standard means well known to the artisan, including filtration, ultrafiltration, electrophoresis, size chromatography, precipitation with specific antibodies, ion exchange chromatography, isoelectrofocusing, and the like.

Sequencing of the isolated peptides can be performed according to standard techniques such as Edman degradation (Hunkapiller, M.W., *et al.*, *Methods Enzymol.* 91, 399 (1983)). Other methods suitable for sequencing include mass spectrometry sequencing of individual peptides as previously described (Hunt, *et al.*, *Science* 225:1261 (1992)). Amino acid sequencing of bulk heterogeneous peptides (*e.g.*, pooled HPLC fractions) from different MHC molecules typically reveals a characteristic sequence motif for each MHC allele. A large number of cells with defined MHC molecules, particularly MHC Class I molecules, are known and readily available. For example, human EBV-transformed B cell lines have been shown to be excellent sources for the preparative isolation of class I and class II MHC molecules. Well-characterized cell lines are available from private and commercial sources, such as American Type Culture Collection ("Catalogue of Cell Lines and Hybridomas," 6th edition (1988) Manassas, Virginia, U.S.A.); National Institute of General Medical Sciences 1990/1991 Catalog of Cell Lines (NIGMS) Human Genetic Mutant Cell Repository, Camden, NJ; and ASHI Repository, Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115. Table 5 lists some B cell lines suitable for use as sources for HLA alleles. All of these cell lines can be grown in large batches and are therefore useful for large scale production of MHC molecules. One of skill will recognize that these are merely exemplary cell lines and that many other cell sources can be employed. Specific cell lines and antibodies used to determine class II and murine peptides disclosed herein are set forth in Tables 8 and 9.

Table 8
HLA Class II MHC molecules

Antigen	HLA-DR,DQ Allele	Cell Line	Ab utilized for Capture assay
DR1	DRB1*0101	LG2	LB3.1
DR3	DRB1*0301	MAT	LB3.1
DR4	DRB1*0401	PREISS	LB3.1
DR4	DRB1*0404	BIN40	LB3.1
DR4	DRB1*0405	KT3	LB3.1
DR7	DRB1*0701	PITOUT, DBB	LB3.1
DR8	DRB1*0802	OLL	LB3.1
DR9	DRB1*0901	HID	LB3.1
DR11	DRB1*1101	SWEIG	LB3.1
DR12	DRB1*1201	HERLUF	LB3.1
DR13	DRB1*1302	H0301	LB3.1
DR15	DRB1*1501	L466.1	LB3.1
DR52	DRB3*0101	MAT	LB3.1
DR53	DRB4*0101	L257.6	LB3.1
DR51	DRB5*0101	GM3107, L416.3	LB3.1
DQ7	DQA1*0301/B*0301	PF	
DQ2	DQA1*0501/B*0201	MAT, STEINLIN	
DQ8	DQA1*0301/B*0302	145b, PREISS, YAR	

Table 9
Murine MHC molecules

MHC class	Allele	Cell Line	Ab utilized for Capture Assay
I	Db	EL4	
I	Db	P815	
I	Kb	EL4	
I	Kd	P815	
I	Kk	CH27	Y3
I	Ld	P815	
II	IAb	DB27.4	
II	IAd	A20	
II	IAk	CH12	
II	IAs	LS102.9	
II	IAu	91.7	
II	IEd	A20	
II	IEk	CH12	

The peptides of the invention can be prepared synthetically, or by recombinant DNA technology or from natural sources such as whole viruses or tumors. Although the peptide will preferably be substantially free of other

naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides can be synthetically or naturally conjugated to native protein fragments or particles. The peptides of the invention can be prepared in a wide variety of ways. Because of their relatively short size, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. See, for example, Stewart and Young, *Solid Phase Peptide Synthesis*, 2d. ed., Pierce Chemical Co. (1984), *supra*.

B. MHC Binding Assays

The capacity to bind MHC molecules is measured in a variety of different ways. One means is a MHC binding assay as described in the related applications, noted above. Other alternatives described in the literature include inhibition of antigen presentation (Sette, *et al.*, *J. Immunol.* 141:3893 (1991), *in vitro* assembly assays (Townsend, *et al.*, Cell 62:285 (1990), and FACS based assays using mutated cells, such as RMA.S (Melief, *et al.*, *Eur. J. Immunol.* 21:2963 (1991)).

Capture Assay: Unlike the HPLC-based molecular binding assay, noted above, the high throughput screening ("HTS") Capture assay does not utilize a size-exclusion silica column for separation of bound from unbound radioactive marker. Instead, wells of an opaque white 96-well Optiplate (Packard) are coated with 3μg (100μl @ 30μg/ml) of HLA-specific antibody (Ab) that "capture" complexes of radiolabeled MHC and unlabeled peptide transferred from the molecular binding assay plate in 100μl of 0.05% NP40/PBS. After a 3-hour incubation period, the supernatant is decanted and scintillation fluid (Microscint 20) added. Captured complexes are then measured on a microplate scintillation and luminescence counter (TopCount NXTTM; Packard).

Additional assays for determining binding are described in detail, *e.g.*, in PCT publications WO 94/20127 and WO 94/03205. Binding data results are often expressed in terms of IC_{50} value. IC_{50} is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide occurs. Given the conditions in which the assays are performed (*e.g.*, limiting

MHC proteins and labeled peptide concentrations), these values approximate K_D values. It should be noted that IC_{50} values can change, often dramatically, if the assay conditions are varied, and depending on the particular reagents used (*e.g.*, MHC preparation, *etc.*). For example, excessive concentrations of MHC molecules will increase the apparent measured IC_{50} of a given ligand. Alternatively, binding is expressed relative to a reference peptide. Although as a particular assay becomes more, or less, sensitive, the IC_{50}'s of the peptides tested may change somewhat, the binding relative to the reference peptide will not significantly change. For example, in an assay preformed under conditions such that the IC_{50} of the reference peptide increases 10-fold, the IC_{50} values of the test peptides will also increase approximately 10-fold. Therefore, to avoid ambiguities, the assessment of whether a peptide is a good, intermediate, weak, or negative binder is generally based on its IC_{50}, relative to the IC_{50} of a standard peptide.

Binding may also be determined using other assay systems including those using: live cells (*e.g.*, Ceppellini *et al.*, *Nature* 339:392, 1989; Christnick *et al.*, *Nature* 352:67, 1991; Busch *et al.*, *Int. Immunol.* 2:443, 19990; Hill *et al.*, *J. Immunol.* 147:189, 1991; del Guercio *et al.*, *J. Immunol.* 154:685, 1995), cell free systems using detergent lysates (*e.g.*, Cerundolo *et al.*, *J. Immunol.* 21:2069, 1991), immobilized purified MHC (*e.g.*, Hill *et al.*, *J. Immunol.* 152, 2890, 1994; Marshall *et al.*, *J. Immunol.* 152:4946, 1994), ELISA systems (*e.g.*, Reay *et al.*, *EMBO J.* 11:2829, 1992), surface plasmon resonance (*e.g.*, Khilko *et al.*, *J. Biol. Chem.* 268:15425, 1993); high flux soluble phase assays (*e.g.*, Hammer *et al.*, *J. Exp. Med.* 180:2353, 1994), and measurement of class I MHC stabilization or assembly (*e.g.*, Ljunggren *et al.*, *Nature* 346:476, 1990; Schumacher *et al.*, *Cell* 62:563, 1990; Townsend *et al.*, *Cell* 62:285, 1990; Parker *et al.*, *J. Immunol.* 149:1896, 1992).

High affinity with respect to HLA class I molecules is defined as binding with an IC_{50}, or K_D value, of 50 nM or less; intermediate affinity with respect to HLA class I molecules is defined as binding with an IC_{50} or K_D value of between about 50 and about 500 nM. High affinity with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or K_D value of 100 nM or less; intermediate affinity with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or K_D value of between

about 100 and about 1000 nM. These values are as previously defined in the related patents and applications cited above.

C. Peptide Compositions

The polypeptides or peptides of the invention can be a variety of lengths, either in their neutral (uncharged) forms or in forms which are salts, and either free of modifications such as glycosylation, side chain oxidation, or phosphorylation or containing one or more of these modifications, subject to the condition that the modification not destroy the biological activity of the polypeptides as herein described.

Desirably, the peptide will be as small as possible while still maintaining substantially all of the biological activity of the large peptide. In one embodiment, it may be desirable to optimize peptides of the invention to a length of 9 or 10 amino acid residues, commensurate in size with endogenously processed viral peptides or tumor cell peptides that are bound to MHC class I molecules on the cell surface. In another embodiment, it may be desirable to optimize peptides of the invention to about 15 to 20 amino acid residues, commensurate with peptides that are bound to MHC class II molecules on the cell surface.

Peptides having the desired activity may be modified as necessary to provide certain desired attributes, *e.g.*, improved pharmacological characteristics, while increasing or at least retaining substantially all of the biological activity of the unmodified peptide to bind the desired MHC molecule and activate the appropriate T cell. For instance, the peptides may be subject to various changes, such as substitutions, either conservative or non-conservative, where such changes might provide for certain advantages in their use, such as improved MHC binding. "Conservative substitution" refers to the replacement of an amino acid residue with another which is biologically and/or chemically similar, *e.g.*, one hydrophobic residue for another, or one polar residue for another. The substitutions include combinations such as Gly, Ala; Val, Ile, Leu, Met; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr. The effect of single amino acid substitutions may also be probed using D-amino acids. Such modifications may be made using well known peptide synthesis procedures, as described in *e.g.*, Merrifield, *Science* 232:341-347

(1986), Barany and Merrifield, *The Peptides*, Gross and Meienhofer, eds. (N.Y., Academic Press), pp. 1-284 (1979); and Stewart and Young, *Solid Phase Peptide Synthesis*, (Rockford, Ill., Pierce), 2d Ed. (1984).

The peptides of the invention can also be modified by extending or decreasing the compound's amino acid sequence, *e.g.*, by the addition or deletion of amino acids. The peptides or analogs of the invention can also be modified by altering the order or composition of certain residues, it being readily appreciated that certain amino acid residues essential for biological activity, *e.g.*, those at critical contact sites or conserved residues, may generally not be altered without an adverse effect on biological activity. The non-critical amino acids need not be limited to those naturally occurring in proteins, such as L-α-amino acids, or their D-isomers, but may include non-natural amino acids as well, such as β-γ-δ-amino acids, as well as many derivatives of L-α-amino acids.

Typically, a series of peptides with single amino acid substitutions are employed to determine the effect of electrostatic charge, hydrophobicity, etc. on binding. For instance, a series of positively charged (*e.g.*, Lys or Arg) or negatively charged (*e.g.*, Glu) amino acid substitutions are made along the length of the peptide revealing different patterns of sensitivity towards various MHC molecules and T cell receptors. In addition, multiple substitutions using small, relatively neutral moieties such as Ala, Gly, Pro, or similar residues may be employed. The substitutions may be homo-oligomers or hetero-oligomers. The number and types of residues which are substituted or added depend on the spacing necessary between essential contact points and certain functional attributes which are sought (*e.g.*, hydrophobicity versus hydrophilicity). Increased binding affinity for an MHC molecule or T cell receptor may also be achieved by such substitutions, compared to the affinity of the parent peptide. In any event, such substitutions should employ amino acid residues or other molecular fragments chosen to avoid, for example, steric and charge interference which might disrupt binding.

Substitutions, deletions, insertions or any combination thereof may be combined to arrive at a final peptide. Substitutional variants are those in which at least one residue of a peptide has been removed and a different residue inserted in its place. Such substitutions generally are made in

accordance with the following Table 10 when it is desired to finely modulate the characteristics of the peptide.

TABLE 10

Original Residue	Exemplary Substitution
Ala	Ser
Arg	Lys, His
Asn	Gln
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Lys; Arg
Ile	Leu; Val
Leu	Ile; Val
Lys	Arg; His
Met	Leu; Ile
Phe	Tyr; Trp
Ser	Thr
Thr	Ser
Trp	Tyr; Phe
Tyr	Trp; Phe
Val	Ile; Leu
Pro	Gly

The peptides may also comprise isosteres of two or more residues in the MHC-binding peptide. An isostere as defined here is a sequence of two or more residues that can be substituted for a second sequence because the steric conformation of the first sequence fits a binding site specific for the second sequence. The term specifically includes peptide backbone modifications well known to those skilled in the art. Such modifications include modifications of the amide nitrogen, the α-carbon, amide carbonyl, complete replacement of the amide bond, extensions, deletions or backbone crosslinks.

See, generally, Spatola, *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, Vol. VII (Weinstein ed., 1983).

Modifications of peptides with various amino acid mimetics or unnatural amino acids are particularly useful in increasing the stability of the peptide *in vivo*. Stability can be assayed in a number of ways. For instance, peptidases and various biological media, such as human plasma and serum, have been used to test stability. *See, e.g.*, Verhoef *et al.*, *Eur. J. Drug Metab. Pharmacokin.* 11:291-302 (1986). Half life of the peptides of the present invention is conveniently determined using a 25% human serum (v/v) assay. The protocol is generally as follows. Pooled human serum (Type AB, non-heat inactivated) is delipidated by centrifugation before use. The serum is then diluted to 25% with RPMI tissue culture media and used to test peptide stability. At predetermined time intervals a small amount of reaction solution is removed and added to either 6% aqueous trichloracetic acid or ethanol. The cloudy reaction sample is cooled (4°C) for 15 minutes and then spun to pellet the precipitated serum proteins. The presence of the peptides is then determined by reversed-phase HPLC using stability-specific chromatography conditions.

The peptides of the present invention or analogs thereof which have CTL and/or HTL stimulating activity may be modified to provide desired attributes other than improved serum half life. For instance, the ability of the peptides to induce CTL activity can be enhanced by linkage to a sequence which contains at least one epitope that is capable of inducing a HTL response. Particularly preferred immunogenic peptides/T helper conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, *e.g.*, Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer. When present, the spacer will usually be at least one or two residues, more usually three to six residues, for example, 3, 4, 5 or 6 residues. Alternatively, the CTL peptide may be linked to the HTL peptide without a spacer. The immunogenic peptide may be linked

to the HTL peptide either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic peptide or the HTL peptide may be acylated. Exemplary HTL peptides include tetanus toxoid 830-843, influenza 307-319, malaria circumsporozoite 382-398 and 378-389.

In addition, additional amino acids can be added to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support, or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or the like, can be introduced at the C- or N-terminus of the peptide or oligopeptide. Modification at the C-terminus in some cases may alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-NH_2 acylation, *e.g.*, by alkanoyl (C_1-C_{20}) or thioglycolyl acetylation, terminal-carboxyl amidation, *e.g.*, ammonia, methylamine, etc. In some instances these modifications may provide sites for linking to a support or other molecule.

Alternatively, recombinant DNA technology may be employed wherein a nucleotide sequence which encodes an immunogenic peptide of interest is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art, as described generally in Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1982). Thus, fusion proteins which comprise one or more peptide sequences of the invention can be used to present the appropriate T cell epitope.

As the coding sequence for peptides of the length contemplated herein can be synthesized by chemical techniques, for example, using the phosphotriester method of Matteucci *et al.*, *J. Am. Chem. Soc.* 103:3185 (1981), with modification made simply by substituting the appropriate base(s) for those encoding the native peptide sequence. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired fusion protein. A number of such vectors and suitable

host systems are now available. For expression of the fusion proteins, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired cellular host. For example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts. Of course, yeast or mammalian cell hosts may also be used, employing suitable vectors and control sequences that are well-known in the art.

The peptide compositions of this invention may encode an MHC epitope operably linked to a MHC targeting sequence. The use of a MHC targeting sequence enhances the immune response to an antigen, relative to delivery of antigen alone, by directing the peptide epitope to the site of MHC molecule assembly and transport to the cell surface, thereby providing an increased number of MHC molecule-peptide epitope complexes available for binding to and activation of T cells. MHC Class I targeting sequences can be used in the present invention, *e.g.*, those sequences that target an MHC Class I epitope peptide to a cytosolic pathway or to the endoplasmic reticulum (*see, e.g.*, Rammensee *et al.*, *Immunogenetics* 41:178-228 (1995)). Such MHC Class I targeting sequences are well known in the art, and include, *e.g.*, signal sequences such as those from Ig, tissue plasminogen activator or insulin. *See, e.g.,* Bonnerot *et al., Immunity* 3:335-347 (1995). A preferred signal peptide is the human Ig kappa chain sequence. Endoplasmic reticulum signal sequences can also be used to target MHC Class II epitopes to the endoplasmic reticulum, the site of MHC Class I molecule assembly. MHC Class II targeting sequences can also be used in the invention, e.g., those that target a peptide to the endocytic pathway. These targeting sequences typically direct extracellular antigens to enter the endocytic pathway, which results in the antigen being transferred to the lysosomal compartment where the antigen is proteolytically cleaved into antigen peptides for binding to MHC Class II molecules. For example, a group of MHC Class II targeting sequences useful in the invention are lysosomal targeting sequences, which localize polypeptides to lysosomes. Lysosomal targeting sequences are well known in

the art and include exemplary sequences as described in U.S. Patent No. 5,633,234 and Copier *et al., J. Immunol.* 157:1017-1027 (1996).

Substantial changes in function (*e.g.*, affinity for MHC molecules or T cell receptors) are made by selecting substitutions that are less conservative than those in Table 10, *e.g.*, selecting residues that differ more significantly in their effect on maintaining (a) the structure of the peptide backbone in the area of the substitution, for example as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in peptide properties will be those in which (a) a hydrophilic residue, *e.g.* seryl, is substituted for (or by) a hydrophobic residue, *e.g.* leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a residue having an electropositive side chain, *e.g.*, lysl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, *e.g.* glutamyl or aspartyl; or (c) a residue having a bulky side chain, *e.g.* phenylalanine, is substituted for (or by) one not having a side chain, *e.g.*, glycine.

Epitopes on any number of potential target proteins can be identified. Examples of suitable antigens include prostate specific antigen (PSA), prostate specific membrane antigen (PSM) hepatitis B virus core and surface antigens (HBVc, HBVs), hepatitis C antigens, malignant melanoma antigens (MAGE-1, MAGE-2, MAGE-3), Epstein-Barr virus antigens, human immunodeficiency type-1 virus (HIV-1), human immunodeficiency virus type-2 (HIV-2), papilloma virus antigens, Lassa virus, mycobacterium tuberculosis (MT) antigens, p53 and murine p53 (mp53) antigens, CEA, HER2/neu, and members of the tyrosine kinase related protein families (TKP). The peptides are thus useful in pharmaceutical compositions for both *in vivo* and *ex vivo* therapeutic and diagnostic applications.

D. Peptide Immunogenicity In Vitro and In Vivo

Peptides comprising the epitopes from these antigens are synthesized and then tested for their ability to bind to the appropriate MHC molecules in assays using, for example, purified MHC molecules and radioiodonated peptides and/or cells expressing empty MHC molecules by, for instance, immunofluorescent staining and flow microfluorometry, peptide-dependent

class I assembly assays, and inhibition of CTL or HTL recognition by peptide competition. Those peptides that bind to the MHC molecule are further evaluated for their ability to serve as targets for CTLs and/or HTLs derived from infected or immunized individuals, as well as for their capacity to induce primary *in vitro* or *in vivo* T cell responses that can give rise to CTL and/or HTL populations capable of reacting with virally infected target cells or tumor cells as potential therapeutic agents.

Since mutant cell lines do not exist for every human MHC allele, it is advantageous to use various techniques to remove endogenous MHC-associated peptides from the surface of antigen presenting cell (APC) (*e.g.*, mild acid treatment) followed by loading the resulting empty MHC molecules with the immunogenic peptides of interest. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells or dendritic cells (Inaba, *et al.*, *J. Exp. Med.* 166:182 (1987); Boog, *Eur. J. Immunol.* 18:219 (1988)). The use of non-transformed (non-tumorigenic), non-infected cells, and preferably, autologous cells of patients as the source of APC is desirable for the design of T cell induction protocols directed towards development of *ex vivo* CTL and/or HTL therapies.

Alternatively, mutant mammalian cell lines that are deficient in their ability to load class I molecules with internally processed peptides, such as the mouse cell lines RMA-S (Kärre, *et al.*, *Nature*, 319:675 (1986); Ljunggren, *et al.*, *Eur. J. Immunol.* 21:2963-2970 (1991)), and the human somatic T cell hybrid, T-2 (Cerundolo, *et al.*, Nature 345:449-452 (1990)) and which have been transfected with the appropriate human class I genes are conveniently used, when peptide is added to them, to test for the capacity of the peptide to induce *in vitro* primary CTL responses. Other eukaryotic cell lines which could be used include various insect cell lines such as mosquito larvae (*e.g.*, ATCC cell lines CCL 125, 126, 1660, 1591, 6585, 6586), silkworm (*e.g.*, ATTC CRL 8851), armyworm (*e.g.*, ATCC CRL 1711), moth (*e.g.*, ATCC CCL 80) and Drosophila cell lines (*e.g.*, a Schneider cell line (*see* Schneider, *J. Embryol. Exp. Morphol.*, 27:353-365 (1927))).

Specificity and MHC restriction of the CTL or HTL is determined by testing against different peptide target cells expressing appropriate or inappropriate MHC molecules. The peptides that test positive in the MHC

binding assays and give rise to specific CTL and/or HTL responses are referred to herein as immunogenic peptides.

Analyses of CTL and HTL responses against the immunogen, as well as against common recall antigens are commonly used and are known in the art. Assays employed included chromium release, lymphokine secretion and lymphoproliferation assays. Assays useful in these determinations are described in *Current Protocols in Immunology*, J.E. Coligan, et al., eds., John Wiley & Sons Press (2000), chapters 3, 4, 6, and 7.

In one embodiment, the appropriate antigen-presenting cells are incubated with 10-100 μM of peptide in serum-free media for 4 hours under appropriate culture conditions. The peptide-loaded antigen-presenting cells are then incubated with the responder cell populations *in vitro* for 7 to 10 days under optimized culture conditions. If screening for MHC class I presented peptides, positive CTL activation can be determined by assaying the cultures for the presence of CTLs that kill radiolabeled target cells, both specific peptide-pulsed targets as well as target cells expressing the endogenously processed form of the relevant virus or tumor antigen from which the peptide sequence was derived. If screening for MHC class II-presented peptides, positive HTL activation can be determined by assaying cultures for cytokine production or proliferation.

In one embodiment, prior to incubation of the stimulator cells with the cells to be activated, *e.g.*, precursor CD8+ cells, an amount of antigenic peptide is added to the stimulator cell culture, of sufficient quantity to become loaded onto the human Class I molecules to be expressed on the surface of the stimulator cells. In the present invention, a sufficient amount of peptide is an amount that will allow about 200, and preferably 200 or more, human Class I MHC molecules loaded with peptide to be expressed on the surface of each stimulator cell. Preferably, the stimulator cells are incubated with >20μg/ml peptide.

Resting or precursor CD8+ cells are then incubated in culture with the appropriate stimulator cells for a time period sufficient to activate the CD8+ cells. Preferably, the CD8+ cells are activated in an antigen-specific manner. The ratio of resting or precursor CD8+ (effector) cells to stimulator cells may vary from individual to individual and may further depend upon variables such

as the amenability of an individual's lymphocytes to culturing conditions and the nature and severity of the disease condition or other condition for which the within-described treatment modality is used. Preferably, however, the lymphocyte:stimulator cell ratio is in the range of about 30:1 to 300:1. The effector/stimulator culture may be maintained for as long a time as is necessary to stimulate a therapeutically useable or effective number of CD8+ cells.

The peptides of the invention can be identified and tested for *in vivo* immunogenicity using HLA transgenic mice. The utility of HLA transgenic mice for the purpose of epitope identification (Sette et al., *J Immunol,* 153:5586-92 (1994); Wentworth et al., *Int Immunol,* 8:651-9 (1996); Engelhard et al., *J Immunol,* 146:1226-32 (1991); Man et al., *Int Immunol,* 7:597-605 (1995); Shirai et al., *J Immunol,* 154:2733-42 (1995)), and vaccine development (Ishioka et al., *J Immunol,* 162:3915-25 (1999)) has been established. Most of the published reports have investigated the use of HLA A2.1/K^b mice but it should be noted that B*27, and B*3501 mice are also available. Furthermore, HLA A*11/K^b mice (Alexander et al., *J. Immunol.,* 159:4753-61 (1997)), and HLA B7/K^b and HLA A1/K^b mice have also been generated. Data from 38 different potential epitopes was analyzed to determine the level of overlap between the A2.1-restricted CTL repertoire of A2.1/K^b-transgenic mice and A2.1+ humans (Wentworth et al., *Eur J Immunol,* 26:97-101 (1996)). In both humans and mice, an MHC peptide binding affinity threshold of approximately 500 nM correlates with the capacity of a peptide to elicit a CTL response *in vivo*. A high level of concordance between the human data *in vivo* and mouse data *in vivo* was observed for 85% of the high-binding peptides, 58% of the intermediate binders, and 83% of the low/negative binders. Similar results were also obtained with HLA A11 and HLA B7 transgenic mice (Alexander et al., *J Immunol,* Vol. 159(10):4753-61 (1997)). Thus, because of the extensive overlap that exists between T cell receptor repertoires of HLA transgenic mouse and human CTLs, transgenic mice are valuable for assessing immunogenicity of the multi-epitope constructs described herein. Peptides binding to MHC class II alleles can be examined using HLA-DR transgenic mice. *See, e.g.,* Taneja V., David C.S., *Immunol Rev,* 169:67-79 (1999)).

More sensitive techniques such as the ELISPOT assay, intracellular cytokine staining, and tetramer staining have become available in the art to determine lymphocyte antigen responsiveness. It is estimated that these newer methods are 10- to 100-fold more sensitive than the common CTL and HTL assays (Murali-Krishna et al., *Immunity,* 8:177-87 (1998)), because the traditional methods measure only the subset of T cells that can proliferate *in vitro*, and may, in fact, be representative of only a fraction of the memory T cell compartment (Ogg G.S., McMichael A.J., *Curr Opin Immunol,* 10:393-6 (1998)). Specifically in the case of HIV, these techniques have been used to measure antigen-specific CTL responses from patients that would have been undetectable with previous techniques (Ogg et al., *Science,* 279:2103-6 (1998); Gray et al., *J Immunol,* 162:1780-8 (1999); Ogg et al., *J Virol,* 73:9153-60 (1999); Kalams et al., *J Virol,* 73:6721-8 (1999); Larsson et al., *AIDS,* 13:767-77 (1999); Corne et al., *J Acquir Immune Defic Syndr Hum Retrovirol,* 20:442-7 (1999)).

The peptides of the present invention and pharmaceutical and vaccine compositions thereof are useful for administration to mammals, particularly humans, to treat and/or prevent viral infection and cancer. Examples of diseases which can be treated using the immunogenic peptides of the invention include prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV and chondyloma acuminatum. A protective (or prophylatic) vaccine includes one that will protect against future exposure to pathogen or cancer. A therapeutic vaccine includes one that will ameliorate, attenuate, or ablate symptoms or disease state induced by or related to a pathogen or malignancy.

In circumstances in which efficacy of a prophylactic vaccine is primarily correlated with the induction of a long-lasting memory response, restimulation assays can be the most appropriate and sensitive measures to monitor vaccine-induced immunological responses. Conversely, in the case of therapeutic vaccines, the main immunological correlate of activity can be the induction of effector T cell function, most aptly measured by primary assays. Thus, the use of sensitive assays allows for the most appropriate testing strategy for immunological monitoring of vaccine efficacy.

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes CTL. Lipids have been identified as agents capable of priming CTL *in vivo* against viral antigens. The lipidated peptide can then be injected directly in a micellar form, incorporated into a liposome or emulsified in an adjuvant, *e.g.*, incomplete Freund's adjuvant.

For pharmaceutical compositions, the immunogenic peptides of the invention are administered to an individual already suffering from cancer or infected with the virus of interest. Those in the incubation phase or the acute phase of infection can be treated with the immunogenic peptides separately or in conjunction with other treatments, as appropriate. In therapeutic applications, compositions are administered to a patient in an amount sufficient to elicit an effective CTL and/or HTL response to the virus or tumor antigen and to cure or at least partially arrest symptoms and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, *e.g.*, the peptide composition, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician, but generally range for the initial immunization (that is for therapeutic or prophylactic administration) from about 1.0 μg to about 5000 μg of peptide for a 70 kg patient, (*e.g.*, 1.0 μg, 1.5 μg, 2.0 μg, 2.5 μg, 3.0 μg, 3.5 μg, 4.0 μg, 4.5 μg, 5.0 μg, 7.5 μg, 10 μg, 12.5 μg, 15 μg, 17.5 μg, 20 μg, 25 μg, 30 μg, 35 μg, 40 μg, 45 μg, 50 μg, 75 μg, 100 μg, 250 μg, 500 μg, 750 μg, 1000 μg, 1500 μg, 2000 μg, 2500 μg, 3000 μg, 3500 μg, 4000 μg, 4500 μg or 5000 μg), followed by boosting dosages of from about 1.0 μg to about 1000 μg of peptide (*e.g.*, 1.0 μg, 2.0 μg, 2.5 μg, 3.0 μg, 3.5 μg, 4.0 μg, 4.5 μg, 5.0 μg, 7.5 μg, 10 μg, 12.5 μg, 15 μg, 17.5 μg, 20 μg, 25 μg, 30 μg, 35 μg, 40 μg, 45 μg, 50 μg, 75 μg, 100 μg, 250 μg, 500 μg, 750 μg, 1000 μg, 1500 μg, 2000 μg, 2500 μg, 3000 μg, 3500 μg, 4000 μg, 4500 μg or 5000 μg) pursuant to a boosting regimen over weeks to months depending upon the patient's response and condition by measuring specific T cell activity in the patient's blood. It must be kept in mind that the peptides and compositions of the present invention may generally be employed in serious disease states, that is, life-threatening or potentially life threatening

situations. In such cases, in view of the minimization of extraneous substances and the relative nontoxic nature of the peptides, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions.

The peptide compositions can also be used for the treatment of chronic infection and to stimulate the immune system to eliminate virus-infected cells in carriers. It is important to provide an amount of immuno-potentiating peptide in a formulation and mode of administration sufficient to effectively stimulate an appropriate response. Thus, for treatment of chronic infection, a representative dose is in the range of about 1.0 μg to about 5000 μg, preferably about 5 μg to 1000 μg (*e.g.*, 5.0 μg, 7.5 μg, 10 μg, 12.5 μg, 15 μg, 17.5 μg, 20 μg, 25 μg, 30 μg, 35 μg, 40 μg, 45 μg, 50 μg, 75 μg, 100 μg, 250 μg, 300 μg, 350 μg, 400 μg, 450 μg, 500 μg, 550 μg, 600 μg, 650 μg, 700 μg, 750 μg, 800 μg, 900 μg, 950 μg, or 1000 μg,) for a 70 kg patient per dose. Immunizing doses followed by boosting doses at established intervals, *e.g.*, from one to four weeks, may be required, possibly for a prolonged period of time to effectively immunize an individual. In the case of chronic infection, administration should continue until at least clinical symptoms or laboratory tests indicate that the viral infection has been eliminated or substantially abated and for a period thereafter.

The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral or local administration. Preferably, the pharmaceutical compositions are administered parenterally, *e.g.*, intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, *e.g.*, water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such

as pH adjusting and buffering agents, tonicity adjusting agents, wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

A pharmaceutical composition of the invention may comprise one or more T cell stimulatory peptides of the invention. For example, a pharmaceutical composition may comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more T cell stimulatory peptides of the invention. Moreover, a pharmaceutical composition of the invention may comprise one or more T cell stimulatory peptides of the invention in combination with one or more other T cell stimulatory peptides. The concentration of each unique T cell stimulatory peptide of the invention in the pharmaceutical formulations can vary widely, *e.g.*, from less than about 0.001%, about 0.002%, about 0.003%, about 0.004%, about 0.005%, about 0.006%, 0.007%, 0.008%, 0.009%, about 0.01%, about 0.02%, about 0.025%, about 0.03%, about 0.04%, about 0.05%, about 0.06%, about 0.07%, about 0.08%, about 0.09%, about 0.1%, about 0.2%, about 0.3%, about 0.4%, about 0.5%, about 0.6%, about 0.7%, about 0.8%, about 0.9%, about 1%, about 1.1%, about 1.2%, about 1.3%, about 1.4%, about 1.5%, about 1.6%, about 1.7%, about 1.8%, about 1.9%, about 2%, about 3%, about 4%, about 5%, about 6%, about 7%, about 8%, about 9%, about 10%, about 20%, to about 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, etc., in accordance with the particular mode of administration selected. In a preferred embodiment, the concentration of each unique T cell stimulatory peptide of the invention in the pharmaceutical formulations is about 0.001%, about 0.002%, about 0.003%, about 0.004%, about 0.005%, about 0.006%, 0.007%, 0.008%, 0.009%, about 0.01%, about 0.02%, about 0.025%, about 0.03%, about 0.04%, about 0.05%, about 0.06%, about 0.07%, about 0.08%, about 0.09%, about 0.1%, about 0.2%, about 0.3%, about 0.4%, about 0.5%, about 0.6%, about 0.7%, about 0.8%, about 0.9%, about 1% by weight. In a more preferred embodiment, the concentration of each unique T cell stimulatory peptide of the invention in the pharmaceutical formulations is about 0.01%, about 0.02%, about 0.025%,

about 0.03%, about 0.04%, about 0.05%, about 0.06%, about 0.07%, about 0.08%, about 0.09%, about 0.1% by weight.

The peptides of the invention may also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or targeted selectively to infected cells, as well as increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to, *e.g.*, a receptor prevalent among lymphoid cells, such as monoclonal antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the selected therapeutic/immunogenic peptide compositions. Liposomes for use in the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, *e.g.*, liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, *e.g.*, Szoka *et al.*, *Ann. Rev. Biophys. Bioeng.* 9:467 (1980), U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369, each of which is incorporated herein by reference.

For targeting to the immune cells, a ligand to be incorporated into the liposome can include, *e.g.*, antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, etc. in a dose which varies according to, inter alia, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a

pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are 0.01%-20% by weight, preferably 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, as desired, as with, *e.g.*, lecithin for intranasal delivery.

In another aspect the present invention is directed to vaccines which contain as an active ingredient an immunogenically effective amount of an immunogenic peptide as described herein. The peptide(s) may be introduced into a host, including humans, linked to its own carrier or as a homopolymer or heteropolymer of active peptide units. Such a polymer has the advantage of increased immunological reaction and, where different peptides are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that react with different antigenic determinants of the virus or tumor cells. Useful carriers are well known in the art, and include, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly(lysine:glutamic acid), influenza, hepatitis B virus core protein, hepatitis B virus recombinant vaccine and the like. The vaccines can also contain a physiologically tolerable (acceptable) diluent such as water, phosphate buffered saline, or saline, and further typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant ("IFA"), aluminum phosphate, aluminum hydroxide, or alum are materials well known in the art. And, as mentioned above, CTL responses can be primed by conjugating peptides of the invention to lipids, such as P_3CSS. Upon immunization with a

peptide composition as described herein, via injection, aerosol, oral, transdermal or other route, the immune system of the host responds to the vaccine by producing large amounts of CTLs specific for the desired antigen, and the host becomes at least partially immune to later infection, or resistant to developing chronic infection.

Vaccine compositions containing the peptides of the invention are administered to a patient susceptible to or otherwise at risk of viral infection or cancer to elicit an immune response against the antigen and thus enhance the patient's own immune response capabilities. Such an amount is defined to be an "immunogenically effective dose." In this use, the precise amounts again depend on the patient's state of health and weight, the mode of administration, the nature of the formulation, etc., but generally range from about 1.0 μg to about 5000 μg per 70 kilogram patient, more commonly from about 10 μg to about 500 μg per 70 kg of body weight (*e.g.*, 10 μg, 15 μg, 20 μg, 25 μg, 30 μg, 35 μg, 40 μg, 45 μg, 50 μg, 60 μg, 70 μg, 80 μg, 90 μg, 100 μg, 125 μg, 150 μg, 175 μg, 200 μg, 225 μg, 250 μg, 275 μg, 300 μg, 325 μg, 375 μg, 400 μg, 425 μg, 450 μg, 475 μg or 500 μg per 70kg of body weight).

For therapeutic or immunization purposes, nucleic acids encoding one or more of the peptides of the invention can also be administered to the patient. A number of methods are conveniently used to deliver the nucleic acids to the patient. For instance, the nucleic acid can be delivered directly, as "naked DNA". This approach is described, for instance, in Wolff *et. al., Science* 247: 1465-1468 (1990) as well as U.S. Patent Nos. 5,580,859 and 5,589,466. The nucleic acids can also be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Particles comprised solely of DNA can be administered. Alternatively, DNA can be adhered to particles, such as gold particles. The nucleic acids can also be delivered complexed to cationic compounds, such as cationic lipids. Lipid-mediated gene delivery methods are described, for instance, in WO 96/18372; WO 93/24640; Mannino and Gould-Fogerite (1988) *BioTechniques* 6(7): 682-691; Rose U.S. Pat No. 5,279,833; WO 91/06309; and Felgner *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84: 7413-7414. The peptides of the invention can also be expressed by attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus as a vector to express nucleotide

sequences that encode the peptides of the invention. Upon introduction into an acutely or chronically infected host or into a noninfected host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits a host CTL response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848, incorporated herein by reference. Another suitable vector is BCG (Bacille Calmette Guerin). BCG vectors are described, *e.g.*, in Stover, *et al.*, (*Nature* 351:456-460 (1991)). A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, *e.g.*, *Salmonella* typhi vectors and the like, will be apparent to those skilled in the art from the description herein.

A preferred means of administering nucleic acids encoding the peptides of the invention uses minigene constructs encoding multiple epitopes of the invention. To create a DNA sequence encoding the selected CTL epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes are reverse translated. A human codon usage table is used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences, including DNA sequence encoding a variety of spacers between none, some or all DNA sequence encoding peptides, are adjoined to create, a continuous polypeptide sequence. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequence that could be reverse translated and included in the minigene sequence include: helper T lymphocyte epitopes, a leader (signal) sequence, and an endoplasmic reticulum retention signal. In addition, MHC presentation of CTL epitopes may be improved by including synthetic (*e.g.* poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL epitopes.

In some embodiments, a bicistronic expression vector, to allow production of the minigene-encoded epitopes and a second protein included to enhance or decrease immunogenicity can be used. Examples of proteins or polypeptides that could beneficially enhance the immune response if co-expressed include cytokines (*e.g.*, IL2, IL12, GM-CSF), cytokine-inducing molecules (*e.g.*, LeIF) or costimulatory molecules. Helper (HTL) epitopes could be joined to intracellular targeting signals and expressed separately from

the CTL epitopes. This would allow direction of the HTL epitopes to a cell compartment different than the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the MHC class II pathway, thereby improving CTL induction. In contrast to CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (*e.g.*, TGF-β) may be beneficial in certain diseases.

The immunogenic peptides of this invention may also be used to make monoclonal antibodies. Such antibodies may be useful as potential diagnostic or therapeutic agents.

The peptides are also useful as diagnostic reagents (*e.g.*, tetramer reagents; Beckman Coulter, San Diego, CA). For example, a peptide of the invention may be used to determine the susceptibility of a particular individual to a treatment regimen which employs the peptide or related peptides, and thus may be helpful in modifying an existing treatment protocol or in determining a prognosis for an affected individual. In addition, the peptides may also be used to predict which individuals will be at substantial risk for developing chronic infection.

The present invention relates to the determination of allele-specific peptide motifs for human and murine MHC allele subtypes. These motifs are then used to define T cell epitopes from any desired antigen, particularly those associated with human viral diseases, cancers or autoimmune diseases, for which the amino acid sequence of the potential antigen or autoantigen targets is known. The contents of all documents cited above are expressly incorporated herein by reference.

Brief Description of Tables 11-29

Table 11. Identified HLA-A1 allele-binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., number of amino acids in peptide (AA), origin of peptide (organism), identity of originating protein, position of peptide within protein sequence, and analog status, wherein an analog is a peptide of the invention where the amino acid sequence of any naturally-occurring peptide sequence has been modified by substitution of one or more amino acid residues.

Table 12. Binding affinity of HLA-A1 binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., and binding affinity to the designated HLA-A1 alleles (expressed as an IC_{50}).

Table 13. Identified HLA-A2 allele-binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., number of amino acids in peptide (AA), origin of peptide (organism), identity of originating protein, position of peptide within protein sequence, and analog status, wherein an analog is a peptide of the invention where the amino acid sequence of any naturally-occurring peptide sequence has been modified by substitution of one or more amino acid residues.

Table 14. Binding affinity of HLA-A2 binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., and binding affinity to the designated HLA-A2 alleles (expressed as an IC_{50}).

Table 15. Identified HLA-A3 allele-binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., number of amino acids in peptide (AA), origin of peptide (organism), identity of originating protein, position of peptide within protein sequence, and analog status, wherein an analog is a peptide of the invention where the amino acid sequence of any naturally-occurring peptide sequence has been modified by substitution of one or more amino acid residues.

Table 16. Binding affinity of HLA-A3 binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., and binding affinity to the designated HLA-A3 alleles (expressed as an IC_{50}).

Table 17. Identified HLA-A24 allele-binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., number of amino acids in peptide (AA), origin of peptide (organism), identity of originating protein, position of peptide within protein sequence, and analog status, wherein an analog is a peptide of the invention where the amino acid sequence of any naturally-occurring peptide sequence has been modified by substitution of one or more amino acid residues.

Table 18. Binding affinity of HLA-A24 binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., and binding affinity to the designated HLA-A24 alleles (expressed as an IC_{50}).

Table 19. Identified HLA-B7 allele-binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., number of amino acids in peptide (AA), origin of peptide (organism), identity of originating protein, position of peptide within protein sequence, and analog status, wherein an analog is a peptide of the invention where the amino acid sequence of any naturally-occurring peptide sequence has been modified by substitution of one or more amino acid residues.

Table 20. Binding affinity of HLA-B7 binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., and binding affinity to the designated HLA-B7 alleles (expressed as an IC_{50}).

Table 21. Identified HLA-B44 allele-binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., number of amino acids in peptide (AA), origin of peptide (organism), identity of originating protein, position of peptide within protein sequence, and analog status, wherein an analog is a peptide of the invention where the amino acid sequence of any naturally-occurring peptide sequence has been modified by substitution of one or more amino acid residues.

Table 22. Binding affinity of HLA-B44 binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., and binding affinity to the designated HLA-B44 alleles (expressed as an IC_{50}).

Table 23. Identified HLA-DQ allele-binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., number of amino acids in peptide (AA), origin of peptide (organism), identity of originating protein, position of peptide within protein sequence, and analog status, wherein an analog is a peptide of the invention where the amino acid sequence of any naturally-occurring peptide sequence has been modified by substitution of one or more amino acid residues.

Table 24. Binding affinity of HLA-DQ binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., and binding affinity to the designated HLA-DQ alleles (expressed as an IC_{50}).

Table 25. Identified HLA-DR allele-binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., number of amino acids in peptide (AA), origin of peptide (organism), identity of originating protein, position of peptide within protein sequence, and analog status, wherein an

analog is a peptide of the invention where the amino acid sequence of any naturally-occurring peptide sequence has been modified by substitution of one or more amino acid residues.

Table 26. Binding affinity of HLA-DR binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., and binding affinity to the designated HLA-DR alleles (expressed as an IC_{50}).

Table 27. Binding affinity of HLA-DR binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., and binding affinity to the designated HLA-DR alleles (expressed as an IC_{50}).

Table 28. Identified murine MHC class I allele-binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., number of amino acids in peptide (AA), origin of peptide (organism), identity of originating protein, position of peptide within protein sequence, and analog status, wherein an analog is a peptide of the invention where the amino acid sequence of any naturally-occurring peptide sequence has been modified by substitution of one or more amino acid residues.

Table 29. Binding affinity of murine MHC class I-binding peptides. Peptides are identified by amino acid sequence, SEQ ID NO., and binding affinity to the designated murine MHC class I alleles (expressed as an IC_{50}).

TABLE 11

HLA-A1 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
AYGPGPGKF		9	Artificial sequence	Consensus		A
AEIPYLAKY		9	Artificial sequence	pool consensus		A
AADAAAAKY		9	Artificial sequence			PolyA
AYSSWMYSY		9	EBV	EBNA3	176	
LAEKTMKEY		9	FluA	POL2	16	
GTYDYWAGY		9	Gonorrhea			
LSVHSIQNDY		10	Gonorrhea			
DTGQCPELVY		10	Gonorrhea			
DLLDTASALY		10	HBV	Core	419	
WFHISCLTF		9	HBV	NUC	102	
LSLDVSAAFY		10	HBV	pol	426	
LSGPGPGAFY		10	HBV	pol	426	A
LSLGPGPGFY		10	HBV	pol	426	A
LSLDGPGPGY		10	HBV	pol	426	A
KTYGRKLHLY		10	HBV	pol	1098	
KTGPGPGHLY		10	HBV	pol	1098	A
KTYGPGPGLY		10	HBV	pol	1098	A
KTYGGPGPGY		10	HBV	pol	1098	A
KYTSFPWL		8	HBV	pol	745	
FAAPFTQCGY		10	HBV	pol	631	
SYQHFRKLLL		10	HBV	POL	4	
LYSHPIILGF		10	HBV	POL	492	
MSTTDLEAY		9	HBV	X	103	
MYVGGPGPGVF		11	HCV	E1	275	A
VMGSSYGF		8	HCV	NS5	2639	
EVDGVRLHRY		10	HCV	NS5	2129	
RTEILDLWVY		10	HIV	NEF	182	A
RQDILDLWVY		10	HIV	NEF	182	A
RTDILDLWVY		10	HIV	NEF	182	A
YTDGPGIRY		9	HIV	NEF	207	A
ATELHPEYY		9	HIV	NEF	322	A
DLWVYHTQGYY		11	HIV	NEF	188	A
WVYHTQGYY		9	HIV	NEF	191	A
FFLKEKGGF		9	HIV	NEF	116	A
LYVYHTQGY		9	HIV	NEF	190	A
ITKILYQSNPY		11	HIV	REV	20	A
KTLYQSNPY		9	HIV	REV	22	A
PVDPNLEPY		9	HIV	TAT	3	A
STVKHHMY		8	HIV	VIF	23	A
LSKISEYRHY		10	HPV	E6	70	
ISEYRHYNY		9	HPV	E6	73	
RFHNIRGRW		9	HPV	E6	131	
RFLSKISEY		9	HPV	E6	68	
RFHNISGRW		9	HPV	E6	124	

HLA-A1 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
TLEKLTNTGLY		11	HPV	E6	89	
TLGPGPGTGLY		11	HPV	E6	89	A
TLEGPGPGGLY		11	HPV	E6	89	A
TLEKGPGPGLY		11	HPV	E6	89	A
TLEKLGPGPGY		11	HPV	E6	89	A
TLEKLTNTGLY		11	HPV	E6	89	
TLEKITNTELY		11	HPV	E6	89	
PYGVCIMCLRF		11	HPV	E6	59	
ITDIILECVY		10	HPV	E6	30	A
YSDISEYRHY		10	HPV	E6	77	A
LTDIEITCVY		10	HPV	E6	25	A
YSDIRELRHY		10	HPV	E6	72	A
ELSSALEIPY		10	HPV	E6	14	
ETSSALEIPY		10	HPV	E6	14	A
ELDSALEIPY		10	HPV	E6	14	A
YTKVSEFRWY		10	HPV	E6	70	A
YSDVSEFRWY		10	HPV	E6	70	A
LTDVSIACVY		10	HPV	E6	25	A
FTSRIRELRY		10	HPV	E6	71	A
YSDIRELRYY		10	HPV	E6	72	A
LTDLRLSCVY		10	HPV	E6	26	A
FTSKVRKYRY		10	HPV	E6	72	A
YSDVRKYRYY		10	HPV	E6	73	A
FYSKVSEFRF		10	HPV	E6	69	A
FYSRIRELRF		10	HPV	E6	71	A
PYAVCRVCLF		10	HPV	E6	62	A
ITEYRHYNY		9	HPV	E6	73	A
ISDYRHYNY		9	HPV	E6	73	A
ITEYRHYQY		9	HPV	E6	73	A
ISDYRHYQY		9	HPV	E6	73	A
LTDLLIRCY		9	HPV	E6	99	A
KTDQRSEVY		9	HPV	E6	35	A
AYRDLCIVY		9	HPV	E6	53	A
KYYSKISEY		9	HPV	E6	75	A
KFYSKISEF		9	HPV	E6	75	A
RYHNIRGRW		9	HPV	E6	131	A
RFHNIRGRF		9	HPV	E6	131	A
AYKDLFVVY		9	HPV	E6	48	A
LFVVYRDSF		9	HPV	E6	52	A
RYHNIAGHY		9	HPV	E6	126	A
RFHNIAGHF		9	HPV	E6	126	A
VYGTTLEKF		9	HPV	E6	83	A
AYADLTVVY		9	HPV	E6	46	A
AFADLTVVF		9	HPV	E6	46	A
RYLSKISEY		9	HPV	E6	68	A
RYHNISGRW		9	HPV	E6	124	A

HLA-A1 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
AYKDLCIVY		9	HPV	E6	48	A
RYHSIAGQY		9	HPV	E6	126	A
RFHSIAGQF		9	HPV	E6	126	A
KYLFTDLRI		9	HPV	E6	44	A
KFLFTDLRF		9	HPV	E6	44	A
LYTDLRIVY		9	HPV	E6	46	A
LFTDLRIVF		9	HPV	E6	46	A
RFLSKISEF		9	HPV	E6	68	A
EYRHYQYSF		9	HPV	E6	75	A
RYHNIMGRW		9	HPV	E6	124	A
RFHNIMGRF		9	HPV	E6	124	A
NFACTELKF		9	HPV	E6	47	A
PYAVCRVCF		9	HPV	E6	62	A
LYYSKVRKY		9	HPV	E6	71	A
VYADLRIVY		9	HPV	E6	46	A
VFADLRIVF		9	HPV	E6	46	A
NYSLYGDTF		9	HPV	E6	80	A
RFHNISGRF		9	HPV	E6	124	A
FTDLTIVY		8	HPV	E6	47	
FTDLRIVY		8	HPV	E6	47	
TLEKLTNTGLY		11	HPV	E6	89	
LTDIEITCVY		10	HPV	E6	25	A
LTDVSIACVY		10	HPV	E6	25	A
ITDIILECVY		10	HPV	E6	30	
KTDQRSEVY		9	HPV	E6	35	
FTDLTIVY		8	HPV	E6	47	
YSDIRELRYY		10	HPV	E6	72	A
YTKVSEFRWY		10	HPV	E6	70	A
FTSRIRELRY		10	HPV	E6	71	A
FTSKVRKYRY		10	HPV	E6	72	A
ISDYRHYNY		9	HPV	E6	73	A
ISEYRHYQY		9	HPV	E6	73	
ISDYRHYQY		9	HPV	E6	73	A
EYRHYCYSLY		10	HPV	E6	82	
EYRHYNYSLY		10	HPV	E6	75	
LTDLLIRCY		9	HPV	E6	99	
ETRHYCYSLY		10	HPV	E6	82	A
EYDHYCYSLY		10	HPV	E6	82	A
KTRYYDYSVY		10	HPV	E6	78	A
KYDYYDYSVY		10	HPV	E6	78	A
ETRHYNYSLY		10	HPV	E6	75	A
EYDHYNYSLY		10	HPV	E6	75	A
PTLKEYVLDLY		11	HPV	E7	6	
HTDTPTLHEY		10	HPV	E7	2	A
RTETPTLQDY		10	HPV	E7	2	A
ETDPVDLLCY		10	HPV	E7	20	A

HLA-A1 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
QTEQATSNYY		10	HPV	E7	46	A
ATDNYYIVTY		10	HPV	E7	50	A
LTEYVLDLY		9	HPV	E7	8	A
QTEQATSNY		9	HPV	E7	46	A
RQAKQHTCY		9	HPV	E7	51	
RTAKQHTCY		9	HPV	E7	51	A
HTDTPTLHEY		10	HPV	E7	2	A
RTETPTLQDY		10	HPV	E7	2	A
PTLKEYVLDLY		11	HPV	E7	6	
LTEYVLDLY		9	HPV	E7	8	A
QAEQATSNY		9	HPV	E7	46	
ATSNYYIVTY		10	HPV	E7	50	
ATDNYYIVTY		10	HPV	E7	50	A
RVLPPNWKY		9	Human	40s riboprot S13	132	
RLAHEVGWKY		10	Human	60s ribo prot L13A	139	
AYKKQFSQY		9	Human	60s ribo prot L5	217	
AADNPPAQY		9	Human	CEA	261	A
RSGPGPGNVLY		11	Human	CEA	225	A
RSDGPGPGVLY		11	Human	CEA	225	A
RSDSGPGPGLY		11	Human	CEA	225	A
RSDSVGPGPGY		11	Human	CEA	225	A
SLFVSNHAY		9	Human	fructose biphosphatealdolase	355	
RWGLLLALL		9	Human	Her2/neu	8	
YTGPGPGVY		9	Human	Jchain	102	A
YTAGPGPGY		9	Human	Jchain	102	A
TQDLVQEKY		9	Human	MAGE1	240	
TQGPGPGKY		9	Human	MAGE1	240	A
TQDGPGPGY		9	Human	MAGE1	240	A
EVGPGPGLY		9	Human	MAGE3	161	A
EVDGPGPGY		9	Human	MAGE3	161	A
IYGPGPGLIF		10	Human	MAGE3	195	A
RISGVDRYY		9	Human	NADH ubiqoxidoreductase	53	
IMVLSFLF		8	Pf	CSP	427	
ALFQEYQCY		9	Pf	CSP	18	
LSEYYDXDIY		10	Pf		347	
FQAAESNERY		10	Pf		13	
ELEASISGKY		10	Pf		81	
FVSSIFISFY		10	Pf		255	
KVSDEIWNY		9	Pf		182	
IMNHLMTLY		9	Pf		38	
LIENELMNY		9	Pf		149	
NVDQQNDMY		9	Pf		182	
SSFFMNRFY		9	Pf		309	
QAAESNERY		9	Pf		14	

HLA-A1 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
LEASISGKY		9	Pf		82	
NLALLYGEY		9	Pf		188	
SSPLFNNFY		9	Pf		14	
QNADKNFLY		9	Pf		145	
VSSIFISFY		9	Pf		256	
SYKSSKRDKF		10	Pf		225	
RYQDPQNYEL		10	Pf		21	
DFFLKSKFNI		10	Pf		3	
NYMKIMNHL		9	Pf		34	
TYKKKNNHI		9	Pf		264	
SFFMNRFYI		9	Pf		310	
FYITTRYKY		9	Pf		316	
KYINFINFI		9	Pf		328	
TWKPTIFLL		9	Pf		135	
KYNYFIHFF		9	Pf		216	
HFFTWGTMF		9	Pf		222	
RMTSLKNEL		9	Pf		61	
YYNNFNNNY		9	Pf		77	
GTDEXRNXY		9	Unknown	Naturally processed		A
ETDXXXDRSEY		11	Unknown	Naturally processed		A
FTDVNSXXRY		10	Unknown	Naturally processed		A
VXDPYNXKY		9	Unknown	Naturally processed		A
VADKVHXMY		9	Unknown	Naturally processed		A
ETXXPDWSY		9	Unknown	Naturally processed		A
XTHNXVDXY		9	Unknown	Naturally processed		A

TABLE 12

HLA-A1 SUPERTYPE

Sequence	SEQ ID NO.	A*0101	A*2902	A*3002
AYGPGPGKF			44854	3.2
AEIPYLAKY				144
AADAAAAKY		20		
AYSSWMYSY				4.9
LAEKTMKEY		174		
GTYDYWAGY		141		
LSVHSIQNDY		279		
DTGQCPELVY		129		
DLLDTASALY			74	37
WFHISCLTF		85324	95	75094
LSLDVSAAFY		267	12	7.1
LSGPGPGAFY		25	1383	6.6
LSLGPGPGFY		21	132	8.2
LSLDGPGPGY		266	274	181
KTYGRKLHLY		171	27	1.5
KTGPGPGHLY		29	192	1.3
KTYGPGPGLY		5.7	227	0.96
KTYGGPGPGY		282	228	1.7
KYTSFPWL			>172413	346
FAAPFTQCGY			461	1364
SYQHFRKLLL		>83333	28	3768
LYSHPIILGF		3166	109	1116
MSTTDLEAY			2565	396
MYVGGPGPGVF			89	2870
VMGSSYGF			145	41967
EVDGVRLHRY			14940	113
RTEILDLWVY		99	10204	315
RQDILDLWVY		8995	13928	95
RTDILDLWVY		85	13424	360
YTDGPGIRY		11	562	7911
ATELHPEYY		43	6608	1734
DLWVYHTQGYY		5880	852	16
WVYHTQGYY		703	215	5.6
FFLKEKGGF			3015	141
LYVYHTQGY			216	258
ITKILYQSNPY		>10060	64908	298
KTLYQSNPY		6912	1703	35
PVDPNLEPY		195	13193	7121
STVKHHMY		8132	1760	68
LSKISEYRHY		14306	55190	186
ISEYRHYNY		25	1329	32
RFHNIRGRW		52917	18	58
RFLSKISEY		>40322	34623	23
RFHNISGRW		48564	174	37

HLA-A1 SUPERTYPE

Sequence	SEQ ID NO.	A*0101	A*2902	A*3002
TLEKLTNTGLY		23	991	92
TLGPGPGTGLY		350	1320	7.4
TLEGPGPGGLY		11	2320	40
TLEKGPGPGLY		13	2036	40
TLEKLGPGPGY		269	4473	1962
TLEKLTNTGLY		77	5500	154
TLEKITNTELY		17	8402	3897
PYGVCIMCLRF			69	43722
ITDIILECVY		1.8	7660	505
YSDISEYRHY		3.8	1350	514
LTDIEITCVY		12	540	80
YSDIRELRHY		14	1137	740
ELSSALEIPY		171	6031	4472
ETSSALEIPY		19	12026	7144
ELDSALEIPY		38	82189	38284
YTKVSEFRWY		276	3308	420
YSDVSEFRWY		3.9	1842	1026
LTDVSIACVY		2.9	764	72
FTSRIRELRY		4.4	77	50
YSDIRELRYY		9.4	733	456
LTDLRLSCVY		45	1783	613
FTSKVRKYRY		64	6677	52
YSDVRKYRYY		19	849	794
FYSKVSEFRF			79	18453
FYSRIRELRF			83	12598
PYAVCRVCLF			407	5226
ITEYRHYNY		114	625	418
ISDYRHYNY		16	45	455
ITEYRHYQY		90	1030	526
ISDYRHYQY		13	37	382
LTDLLIRCY		13	6857	5515
KTDQRSEVY		84	200429	1174
AYRDLCIVY			7117	66
KYYSKISEY			702	1.3
KFYSKISEF			73339	306
RYHNIRGRW			122644	15
RFHNIRGRF			346	0.69
AYKDLFVVY			639	1.3
LFVVYRDSF			919	18
RYHNIAGHY			138	0.93
RFHNIAGHF			635	1.4
VYGTTLEKF			75267	220
AYADLTVVY			136	9.3
AFADLTVVF			779	137
RYLSKISEY			4247	1.1
RYHNISGRW			104884	13

HLA-A1 SUPERTYPE

Sequence	SEQ ID NO.	A*0101	A*2902	A*3002
AYKDLCIVY			5205	29
RYHSIAGQY			544	1.4
RFHSIAGQF			481	1.2
KYLFTDLRI			78575	339
KFLFTDLRF			44	152
LYTDLRIVY			4.8	2.1
LFTDLRIVF			164	2649
RFLSKISEF			40103	201
EYRHYQYSF			13707	430
RYHNIMGRW			106990	7.1
RFHNIMGRF			174	1.3
NFACTELKF			46	6826
PYAVCRVCF			5602	316
LYYSKVRKY			1452	28
VYADLRIVY			8.2	8.3
VFADLRIVF			87	24062
NYSLYGDTF			20945	64
RFHNISGRF			572	2.8
FTDLTIVY		16	1275	39043
FTDLRIVY		26	813	8060
TLEKLTNTGLY		174		
LTDIEITCVY		33		
LTDVSIACVY		57		
ITDIILECVY		187		
KTDQRSEVY		41		
FTDLTIVY		34		
YSDIRELRYY		20		
YTKVSEFRWY		204		
FTSRIRELRY		25		
FTSKVRKYRY		37		
ISDYRHYNY		28		
ISEYRHYQY		40		
ISDYRHYQY		28		
EYRHYCYSLY		125	198	3.7
EYRHYNYSLY		111027	956	12
LTDLLIRCY		64		
ETRHYCYSLY		43	755	10
EYDHYCYSLY		110081	799	77
KTRYYDYSVY		2957	87841	0.71
KYDYYDYSVY		186339	5749	11
ETRHYNYSLY		445	5464	29
EYDHYNYSLY		11251	777	93
PTLKEYVLDLY		195	805	408
HTDTPTLHEY		20	1509	54
RTETPTLQDY		11	1987	239
ETDPVDLLCY		6.4	4110	52640

HLA-A1 SUPERTYPE

Sequence	SEQ ID NO.	A*0101	A*2902	A*3002
QTEQATSNYY		11	9576	500
ATDNYYIVTY		7.4	1918	65
LTEYVLDLY		6.0	941	81
QTEQATSNY		14	119081	3247
RQAKQHTCY		>135135	155246	108
RTAKQHTCY		5647	130343	346
HTDTPTLHEY		30		
RTETPTLQDY		40		
PTLKEYVLDLY		426		
LTEYVLDLY		8.0		
QAEQATSNY		132		
ATSNYYIVTY		428		
ATDNYYIVTY		19		
RVLPPNWKY				3.0
RLAHEVGWKY				3.8
AYKKQFSQY				5.3
AADNPPAQY		9.2		
RSGPGPGNVLY		172	11270	6.3
RSDGPGPGVLY		12	13162	12
RSDSGPGPGLY		3.3	11856	4.2
RSDSVGPGPGY		23	31193	33
SLFVSNHAY				1.1
RWGLLLALL			61253	300
YTGPGPGVY		2.7	2015	6.4
YTAGPGPGY		7.0	28	755
TQDLVQEKY		57	33304	3796
TQGPGPGKY		4192	36746	3.2
TQDGPGPGY		381	37093	541
EVGPGPGLY		50	18183	45
EVDGPGPGY		29	25775	5766
IYGPGPGLIF			58	6845
RISGVDRYY				3.0
IMVLSFLF			111	30000
ALFQEYQCY		>42016	149	1032
LSEYYDXDIY		11	1647	489
FQAAESNERY		8958	1780	372
ELEASISGKY		142	21934	463
FVSSIFISFY		118	22	84
KVSDEIWNY		435	230	1.9
IMNHLMTLY		150	1.7	1.8
LIENELMNY		412	3936	169
NVDQQNDMY		47	22173	79057
SSFFMNRFY		239	36	7.5
QAAESNERY		353	24281	3011
LEASISGKY		57792	17824	87
NLALLYGEY		275	138	102

HLA-A1 SUPERTYPE

Sequence	SEQ ID NO.	A*0101	A*2902	A*3002
SSPLFNNFY		117	389	73
QNADKNFLY		3811	24	663
VSSIFISFY		144	1800	55
SYKSSKRDKF			12594	88
RYQDPQNYEL			79717	189
DFFLKSKFNI			47714	491
NYMKIMNHL			45443	110
TYKKKNNHI			21642	162
SFFMNRFYI			200	1022
FYITTRYKY			9.6	7.5
KYINFINFI			25475	55
TWKPTIFLL			21155	306
KYNYFIHFF			319	2.7
HFFTWGTMF			4.0	220
RMTSLKNEL			40270	14
YYNNFNNNY			19	34
GTDEXRNXY		0.67		
ETDXXXDRSEY		2.0		
FTDVNSXXRY		0.20		
VXDPYNXKY		2.3		
VADKVHXMY		2.4		
ETXXPDWSY		11		
XTHNXVDXY		1.4		

TABLE 13

HLA-A2 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
FPFKYAAAV		9	Artificial sequence			A
AMAKAAAAV		9	Artificial sequence			PolyA
AMAKAAAAL		9	Artificial sequence			PolyA
AMAKAAAAT		9	Artificial sequence			PolyA
AXAKAAAAL		9	Artificial sequence			PolyA
FVYGGSKTSL		10	EBNA		508	
ILGPGPGL		8	Flu	M1	59	A
GILGFVFTL		9	Flu	M1	58	
GLIYNRMGAV		10	Flu A	M1	129	
VLMEWLKTRPI		11	Flu A	M1	41	
FLPSDYFPSV		10	HBV	Core	18	A
FLGPGPGPSV		10	HBV	core	18	A
FLPGPGPGSV		10	HBV	core	18	A
FLPSGPGPGV		10	HBV	core	18	A
WLGPGPGFV		9	HBV	env	335	A
WLSGPGPGV		9	HBV	env	335	A
GVLGWSPQV		9	HBV	env	62	A
PVLPIFFCV		9	HBV	env	377	A
VVQAGFFLV		9	HBV	env	177	A
FLLAQFTSAI		10	HBV	Pol	503	
YLLTLWKAGI		10	HBV	pol	147	
YLGPGPGAGI		10	HBV	pol	147	A
YLLGPGPGGI		10	HBV	pol	147	A
YLLTGPGPGI		10	HBV	pol	147	A
HVYSHPIIV		9	HBV	pol	1076	A
FVLSLGIHV		9	HBV	pol	562	A
YVDDVVLGV		9	HBV	pol	538	A
IVRGTSFVYV		10	HBV	pol	773	A
SLGPGPGIAV		10	HIV	env	814	A
SLLGPGPGAV		10	HIV	env	814	A
SLLNGPGPGV		10	HIV	env	814	A
KITPLCVTL		9	HIV	Env	134	A
KLTPLCVTM		9	HIV	Env	134	A
KLTPLCVPL		9	HIV	Env	134	A
KLTPLCVSL		9	HIV	Env	134	A
KLTPLCITL		9	HIV	Env	134	A
QLTPLCVTL		9	HIV	Env	134	A
KLTPRCVTL		9	HIV	Env	134	A
ELTPLCVTL		9	HIV	Env	134	A
QMTFLCVQM		9	HIV	Env	134	A
KMTFLCVQM		9	HIV	Env	134	A
KLTPLCVAL		9	HIV	Env	134	A
KLTPFCVTL		9	HIV	Env	134	A
SLYNTVATL		9	HIV	GAG	77	
VLAEAMSQT		9	HIV	Gag	386	A
VLAEAMSQA		9	HIV	Gag	386	A

HLA-A2 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
VLAEAMSQI		9	HIV	Gag	386	A
ILAEAMSQV		9	HIV	Gag	386	A
VLAEAMSKV		9	HIV	Gag	386	A
VLAEAMSHA		9	HIV	Gag	386	A
ILAEAMSQA		9	HIV	Gag	386	A
VLAEAMSRA		9	HIV	Gag	386	A
VLAEAMATA		9	HIV	Gag	386	A
ILAEAMASA		9	HIV	Gag	386	A
MTHNPPIPV		9	HIV	Gag	271	A
MTNNPPVPV		9	HIV	Gag	271	A
MTSNPPIPV		9	HIV	Gag	271	A
MTSNPPVPV		9	HIV	Gag	271	A
MTSDPPIPV		9	HIV	Gag	271	A
MTGNPPIPV		9	HIV	Gag	271	A
MTGNPPVPV		9	HIV	Gag	271	A
MTGNPAIPV		9	HIV	Gag	271	A
MTGNPSIPV		9	HIV	Gag	271	A
MTANPPVPV		9	HIV	Gag	271	A
SLYNTVATL		9	hiv	gag	77	
QAHCNISRA		9	HIV	gp160	332	
FLKEKGGV		8	HIV	NEF	117	A
GLGAVSRDL		9	HIV	NEF	45	A
GLITSSNTA		9	HIV	NEF	62	A
ALEEEEVGFPV		11	HIV	NEF	83	A
FLKEKGGLEGV		11	HIV	NEF	117	A
FLKEKGGLDGV		11	HIV	NEF	117	A
GLIYSKKRQEV		11	HIV	NEF	173	A
LLYSKKRQEI		10	HIV	NEF	174	A
LLYSKKRQEIL		11	HIV	NEF	174	A
RLDILDLWV		9	HIV	NEF	182	A
EILDLWVYHV		10	HIV	NEF	185	A
ILDLWVYHV		9	HIV	NEF	186	A
ILDLWVYNV		9	HIV	NEF	186	A
WLNYTPGPGT		10	HIV	NEF	204	A
WQNYTPGPGV		10	HIV	NEF	204	A
WLNYTPGPGI		10	HIV	NEF	204	A
YLPGPGIRYPL		11	HIV	NEF	207	A
YTPGPGIRYPV		11	HIV	NEF	207	A
LLFGWCFKL		9	HIV	NEF	221	A
LTFGWCFKV		9	HIV	NEF	221	A
LLFGWCFKLV		10	HIV	NEF	221	A
FGVRPQVPL		9	HIV	nef	84	A
FTVRPQVPL		9	HIV	nef	84	A
FSVRPQVPL		9	HIV	nef	84	A
YLKEPVHGV		9	HIV	pol	476	A
FLKEPVHGV		9	HIV	pol	476	
PVPLQLPPV		9	HIV	REV	74	A
LQLPPLERV		9	HIV	REV	77	A
LLLPPLERLTL		11	HIV	REV	77	A

HLA-A2 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
LQLPPLERLTV		11	HIV	REV	77	A
ILWQVDRM		8	HIV	VIF	9	A
KLGSLQYL		8	HIV	VIF	146	A
KVGSLQYV		8	HIV	VIF	146	A
TLHDLCQAV		9	HPV	E6	11	A
TLQDIVLHL		9	HPV	E7	7	
TLGPGPGHL		9	HPV	E7	7	A
TLQGPGPGL		9	HPV	E7	7	A
TLSFVCPWCV		10	HPV	E7	94	A
TLSFVCPWCA		10	HPV18	E7	93	
RTLHDLCQA		9	HPV33	E6	10	
TLHDLCQAL		9	HPV33	E6	11	
YLSGADLNL		9	Human	CEA	605	A
YLEPGPVTA		9	Human	gp100	280	
LLDGTATLRL		10	Human	gp100	457	
KVYGLSAFV		9	Human	Her2/neu	369	A
IISAVVAIL		9	Human	Her2/neu	654	A
ILSAVVGIL		9	Human	Her2/neu	654	A
IISAVVGFL		9	Human	Her2/neu	654	A
IISAVVGIV		9	Human	Her2/neu	654	A
KISAVVGIL		9	Human	Her2/neu	369	A
KIFAVVGIL		9	Human	Her2/neu	369	A
KIFASVAIL		9	Human	Her2/neu	369	A
ELVSEFSRV		9	Human	Her2/neu	971	A
VLVHPQWVV		9	Human	Kallikrein2	53	A
VLVHPQWVLTV		11	Human	Kallikrein2	53	A
DLMLLRLSEPV		11	Human	Kallikrein2	120	A
PLVCNGVLQGV		11	Human	Kallikrein2	216	A
VLVHPQWVLTV		11	Human	Kallikrein2	53	A
PLVCNGVLQGV		11	Human	Kallikrein2	216	A
QLGPGPGLMEV		11	Human	MAGE3	159	A
QLVGPGPGMEV		11	Human	MAGE3	159	A
QLVFGPGPGEV		11	Human	MAGE3	159	A
QLVFGGPGPGV		11	Human	MAGE3	159	A
ALGIGILTV		9	Human	MART1	27	A
AMGIGILTV		9	Human	MART1	27	A
LLWQPIPV		8	Human	PAP	136	
LLGPGPGV		8	Human	PAP	136	A
VLAKELKFVTL		11	Human	PAP	30	
VLGPGPGFVTL		11	Human	PAP	30	A
VLAGPGPGVTL		11	Human	PAP	30	A
VLAKGPGPGTL		11	Human	PAP	30	A
VLAKEGPGPGL		11	Human	PAP	30	A
TLMSAMTNV		9	Human	PAP	112	A
ILYSAHDTTV		10	Human	PAP	384	A
IVYSAHDTTV		10	Human	PAP	284	A
VTAKELKFV		9	Human	PAP	30	A
ITYSAHDTTV		10	Human	PAP	284	A
SLSLGFLFV		9	Human	PAP		

HLA-A2 SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
SLSLGFLFLV		10	Human	PAP		
LLALFPPEGV		10	Human	PAP		
LVALFPPEGV		10	Human	PAP		
ALFPPEGVSV		10	Human	PAP		
GLHGQDLFGV		10	Human	PAP		
LLPPYASCHV		10	Human	PAP		
LLWQPIPVHV		10	Human	PAP		
MLLRLSEPV		9	Human	PSA	118	A
ALGTTCYV		8	Human	PSA	143	A
VLRLFVCFLI		10	Pf		2	
FLIFHFFLFL		10	Pf		9	
LIFHFFLFLL		10	Pf		10	
FLFLLYILFL		10	Pf		15	
RLPVICSFLV		10	Pf		32	
VICSFLVFLV		10	Pf		35	
FLVFLVFSNV		10	Pf		39	
MMIMIKFMGV		10	Pf		62	
FLLYILFLV		9	Pf		17	
VICSFLVFL		9	Pf		35	
ATYGIIVPV		9	Pf		159	
KIYKIIIWI		9	Pf		9	
YMIKKLLKI		9	Pf		23	
LMTLYQIQV		9	Pf		42	
FMGVIYIMI		9	Pf		68	
FMNRFYITT		9	Pf		312	
YQDPQNYEL		9	Pf		22	
KTWKPTIFL		9	Pf		134	
LLNESNIFL		9	Pf		142	
FIHFFTWGT		9	Pf		220	
VLFLQMMNV		9	Pf		180	
NQMIFVSSI		9	Pf		251	
MIFVSSIFI		9	Pf		253	
SIFISFYLI		9	Pf		258	
RLFEESLGI		9	Pf		293	
ALWGFFPVL		9	Unknown	A2 alloepitope		A
SVYDFFVWL		9		TRP2	180	
FAPGFFPYL		9				
QLFEDKYAL		9				
MLLSVPLLL		9				

TABLE 14

HLA-A2 SUPERTYPE						
Sequence	SEQ ID NO.	A*0201	A*0202	A*0203	A*0206	A*6802
FPFKYAAAV						92
AMAKAAAAV		181	196	6.7	1485	177
AMAKAAAAL		413	123	3.7	18500	320
AMAKAAAAT		15143	12413	84	37000	>26666.67
AXAKAAAAL		>50000	469	3300	37000	>11428.57
FVYGGSKTSL		296				
ILGPGPGL		672	45	530	1262	56099
GILGFVFTL		1.0	10	236	2.1	1395
GLIYNRMGAV		317				
VLMEWLKTRPI		464				
FLPSDYFPSV		8.5	3.3	3.2	2.2	276
FLGPGPGPSV		17	0.80	2.5	55	286
FLPGPGPGSV		98	18	4.0	665	332
FLPSGPGPGV		21	1.2	3.4	64	40
WLGPGPGFV		171	4.1	2.2	530	293
WLSGPGPGV		220	2.5	12	885	24
GVLGWSPQV		22	157	389	28	9428
PVLPIFFCV		8.7	3136	14286	22	1814
VVQAGFFLV		440	79	2503	81	617
FLLAQFTSAI		65	1.9	4.8	148	533
YLLTLWKAGI		20	19	20	40	1388
YLGPGPGAGI		161	1.0	4.2	548	315
YLLGPGPGGI		180	12	3.3	89	2064
YLLTGPGPGI		42	15	59	60	5678
HVYSHPIIV		150	1923	14	1199	123
FVLSLGIHV		45	399	2817	131	112
YVDDVVLGV		18	14	70	16	354
IVRGTSFVYV		50000	5301	69	5398	1217
SLGPGPGIAV		1131	5.3	11	917	281
SLLGPGPGAV		95	17	2.6	642	795
SLLNGPGPGV		65	3.8	14	63	45
KITPLCVTL		461	36	528	59	883
KLTPLCVTM		340	3.6	143	197	6288
KLTPLCVPL		15	0.25	297	135	67
KLTPLCVSL		67	2.4	240	16	5947
KLTPLCITL		1.7	0.27	23	1.7	9155
QLTPLCVTL		64	1.5	57	368	933
KLTPRCVTL		597	150	20	1554	>63492.06
ELTPLCVTL		7190	38	231	1919	32
QMTFLCVQM		3153	40	1127	232	1297
KMTFLCVQM		1793	22	525	100	8744
KLTPLCVAL		209	2.3	54	11	13009
KLTPFCVTL		87	0.37	28	78	11814
SLYNTVATL		290	6573	68	37000	20000
VLAEAMSQT		290	2.2	0.65	236	447

HLA-A2 SUPERTYPE						
Sequence	SEQ ID NO.	A*0201	A*0202	A*0203	A*0206	A*6802
VLAEAMSQA		24	1.1	0.30	9.6	271
VLAEAMSQI		71	0.15	0.87	70	207
ILAEAMSQV		38	1.1	1.1	101	34
VLAEAMSKV		230	1.8	1.4	93	329
VLAEAMSHA		149	1.7	1.2	121	431
ILAEAMSQA		29	1.0	1.1	8.6	253
VLAEAMSRA		127	0.88	1.0	20	229
VLAEAMATA		6.7	1.4	0.73	8.6	33
ILAEAMASA		22	0.72	0.82	6.8	343
MTHNPPIPV		167	119	1.4	158	1.4
MTNNPPVPV		86	18	0.42	287	309
MTSNPPIPV		53	16	0.39	250	3.8
MTSNPPVPV		22	29	0.80	81	1.1
MTSDPPIPV		107	13	0.45	587	2.5
MTGNPPIPV		125	11	0.74	79	7.8
MTGNPPVPV		2021	158	23	35	0.84
MTGNPAIPV		1200	24	10	213	0.48
MTGNPSIPV		16	1.1	0.43	257	0.57
MTANPPVPV		20	5.0	0.62	134	4.0
SLYNTVATL		367	79	19	15072	247113
QAHCNISRA		338				
FLKEKGGV		13327	653	267	>14341.09	>19464.72
GLGAVSRDL		18679	436	1733	>10393.26	>16666.67
GLITSSNTA		5800	102	64	7865	>14311.27
ALEEEEVGFPV		2420	487	15744	2988	>13793.1
FLKEKGGLEGV		322	3.5	6.8	739	1252
FLKEKGGLDGV		332	3.7	11	3207	3807
GLIYSKKRQEV		8971	57	152	>8564.81	>14260.25
LLYSKKRQEI		80687	382	152	>9438.78	>15686.27
LLYSKKRQEIL		>38167.94	282	1569	>8564.81	>14260.25
RLDILDLWV		43	615	1639	2635	>17777.78
EILDLWVYHV		496	569	1865	2229	163
ILDLWVYHV		17	30	156	145	7414
ILDLWVYNV		40	30	201	135	5814
WLNYTPGPGT		547	124	231	>31623.93	11808
WQNYTPGPGV		1175	114	230	223	11993
WLNYTPGPGI		135	4.6	46	>31623.93	1196
YLPGPGIRYPL		1026	20	1583	3497	782
YTPGPGIRYPV		7764	1985	11126	1112	9.2
LLFGWCFKL		18	4.1	198	340	1084
LTFGWCFKV		15	33	1168	187	9.7
LLFGWCFKLV		658	84	114	1669	3276
FGVRPQVPL						321
FTVRPQVPL						13
FSVRPQVPL						52
YLKEPVHGV		54	0.65	1.9	212	63
FLKEPVHGV		44	0.28	1.9	140	135

HLA-A2 SUPERTYPE						
Sequence	SEQ ID NO.	A*0201	A*0202	A*0203	A*0206	A*6802
PVPLQLPPV		10047	>7337.88	12595	81	>15625
LQLPPLERV		7951	7705	13517	203	1786
LLLPPLERLTL		34	2607	9010	45	>12779.55
LQLPPLERLTV		159	4545	6270	52	>61068.7
ILWQVDRM		1745	67	2998	11332	>19464.72
KLGSLQYL		1862	14	298	9010	>19464.72
KVGSLQYV		1650	441	703	1904	17480
TLHDLCQAV		331	17	15	10585	2809
TLQDIVLHL		22	4.4	46	781	5088
TLGPGPGHL		14974	35	66	12144	27910
TLQGPGPGL		6248	62	951	9121	3809
TLSFVCPWCV		786	123	370	4357	388
TLSFVCPWCA		1611	221	521	27321	13228
RTLHDLCQA		8121	34	678	96	61604
TLHDLCQAL		1404	2.7	40	2182	70390
YLSGADLNL		36	4.9	9.2	1605	51227
YLEPGPVTA		466	10	27	20720	>470588.24
LLDGTATLRL		180	1.9	201	841	>421052.63
KVYGLSAFV		33	1.8	11	69	110
IISAVVAIL		1127	8.0	45	1440	148
ILSAVVGIL		1464	1.9	21	2539	11854
IISAVVGFL		747	1.0	4.8	234	77
IISAVVGIV		712	15	20	958	390
KISAVVGIL		6238	42	60	1752	4952
KIFAVVGIL		3957	38	34	1539	6659
KIFASVAIL		1062	16	21	1068	363
ELVSEFSRV		8178	969	53	197	23
VLVHPQWVV		464	65	1988	3224	14606
VLVHPQWVLTV		11	1.7	3.0	13	3288
DLMLLRLSEPV		69	66	32	118	2078
PLVCNGVLQGV		91	424	36	212	3532
VLVHPQWVLTV		11	1.5	16	31	8889
PLVCNGVLQGV		26	126	19	264	4211
QLGPGPGLMEV		194	9.4	29	481	648
QLVGPGPGMEV		865	17	19	919	223
QLVFGPGPGEV		2944	106	50	4067	447
QLVFGGPGPGV		2153	96	242	3207	1318
ALGIGILTV		11				
AMGIGILTV		15				
LLWQPIPV		137	2445	9.9	4251	32939
LLGPGPGV		25	49	123	93	5620
VLAKELKFVTL		1298	23	194	5170	15664
VLGPGPGFVTL		1528	13	63	4766	42136
VLAGPGPGVTL		1118	2.4	94	7200	2645
VLAKGPGPGTL		11256	26	344	11450	>170212.7

HLA-A2 SUPERTYPE						
Sequence	SEQ ID NO.	A*0201	A*0202	A*0203	A*0206	A*6802
VLAKEGPGPGL		1890	6.9	37	59024	50993
TLMSAMTNV		636	14	35	2188	484
ILYSAHDTTV		397	1.1	13	1480	6285
IVYSAHDTTV		7643	91	627	356	737
VTAKELKFV		7143	2688	40	137	26667
ITYSAHDTTV		4167	115	238	154	82
SLSLGFLFV		77	25	21	93	26667
SLSLGFLFLV		1.9	3.9	17	42	348
LLALFPPEGV		5.0	0.73	1.6	148	163
LVALFPPEGV		156	17	4.8	463	28
ALFPPEGVSV		15	1.1	18	119	4444
GLHGQDLFGV		12	2.3	3.1	18	>80000
LLPPYASCHV		88	15	16	97	5333
LLWQPIPVHV		25	1.8	18	285	62
MLLRLSEPV		47	29	48	689	433
ALGTTCYV		93	6.7	12	292	28284
VLRLFVCFLI		2744	2112	299	68226	45639
FLIFHFFLFL		161	174	2087	288	475
LIFHFFLFLL		200	1468	3167	1562	460
FLFLLYILFL		2834	172	2012	2113	8248
RLPVICSFLV		12	2.5	33	19	9176
VICSFLVFLV		167	415	2916	197	1949
FLVFLVFSNV		269	212	35	232	5393
MMIMIKFMGV		123	19	25	109	39
FLLYILFLV		346	279	3091	1801	6981
VICSFLVFL		184	19	2331	236	4800
ATYGIIVPV		3.2	2.0	2.8	5.0	21
KIYKIIIWI		157	1179	638	101	2198
YMIKKLLKI		105	4.6	4.7	93	63127
LMTLYQIQV		14	1.6	20	615	1276
FMGVIYIMI		13	2.1	26	98	14501
FMNRFYITT		101	18	13	996	6543
YQDPQNYEL		79	18	441	52	166775
KTWKPTIFL		135	1242	7487	76	3617
LLNESNIFL		43	2.5	24	143	4484
FIHFFTWGT		80	4.7	64	60	383
VLFLQMMNV		31	1.8	2.7	9.5	323
NQMIFVSSI		250	21	3.6	14	198
MIFVSSIFI		85	18	83	114	5.2
SIFISFYLI		289	35	1416	43	18
RLFEESLGI		26	1.9	5.5	68	418
ALWGFFPVL		3.6	0.74	3.7	15	1503
SVYDFFVWL		36	169	226	10	0.86
FAPGFFPYL		48	0.85	44	2.3	7.6
QLFEDKYAL		646	1.8	380	2009	2982
MLLSVPLLL		9.0	79	41	8.4	24607

TABLE 15

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
ALNAAAAAK		9	Artificial sequence			Poly
ALAAGAAAK		9	Artificial sequence			Poly
ALQAAAAAK		9	Artificial sequence			Poly
STGPGPGVVRR		11	HBV	core	141	A
STLGPGPGVRR		11	HBV	core	141	A
STLPGPGPGRR		11	HBV	core	141	A
STLPEGPGPGR		11	HBV	core	141	A
QAGFFLLTR		9	HBV	ENV	179	
RVHFASPLH		9	HBV	POL	818	
AAYAAQGYK		9	HCV	II	1247	
KSKFGYGAK		9	HCV	II	2551	
PAAYAAQGYK		10	HCV	II	1246	
RMYVGGVEH		9	HCV	IV	635	
SQLSAPSLK		9	HCV	IV	2209	
TSCGNTLTCY		10	HCV	NS5	2740	
VTGPGPGPVWK		11	HIV	env	48	A
VTVGPGPGVWK		11	HIV	env	48	A
VTVYGPGPGWK		11	HIV	env	48	A
VTVYYGPGPGK		11	HIV	env	48	A
PVRPQVPLR		9	HIV	NEF	95	
HGAITSSNTK		10	HIV	NEF	61	A
AVDLSFFLK		9	HIV	NEF	111	A
DVSHFLKEK		9	HIV	NEF	113	A
GVLDGLIYSK		10	HIV	NEF	124	A
GVDGLIYSK		9	HIV	NEF	125	A
EILDLWVYK		9	HIV	NEF	185	A
ILDLWVYK		8	HIV	NEF	186	A
RVPLTFGWCFK		11	HIV	NEF	216	A
QVYTPGPGTR		10	HIV	NEF	205	A
AVGPGPGLK		9	HIV	nef	84	A
AVDGPGPGK		9	HIV	nef	84	A
QMGPGPGNFK		10	HIV	pol	1432	A
QMAGPGPGFK		10	HIV	pol	1432	A
QMAVGPGPGK		10	HIV	pol	1432	A
TVGPGPGPEK		10	HIV	pol	935	A
TVQGPGPGEK		10	HIV	pol	935	A
TVQPGPGPGK		10	HIV	pol	935	A
VAIKIGGQLK		10	HIV	Pol	98	A
VTVKIGGQLK		10	HIV	Pol	98	A
VTIKVGGQLK		10	HIV	Pol	98	A
VTIRIGGQLK		10	HIV	Pol	98	A
VTVRIGGQLK		10	HIV	Pol	98	A
VTVKVGGQLK		10	HIV	Pol	98	A
VTIRVGGQLK		10	HIV	Pol	98	A

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
VTVRVGGQLK		10	HIV	Pol	98	A
VTVKIGGQLR		10	HIV	Pol	98	A
VTIRIGGQLR		10	HIV	Pol	98	A
VTIKLGGQIR		10	HIV	Pol	98	A
VSIKVGGQIK		10	HIV	Pol	98	A
VSIRVGGQIK		10	HIV	Pol	98	A
VTVKIEGQLK		10	HIV	Pol	98	A
VTIKIEGQLK		10	HIV	Pol	98	A
VTVKIEGQLR		10	HIV	Pol	98	A
VSIRVGGQTK		10	HIV	Pol	98	A
VSIRVGGQTR		10	HIV	Pol	98	A
VTVRIGGMQK		10	HIV	Pol	98	A
ITVKIGKEVR		10	HIV	Pol	98	A
GTRQARRNK		9	HIV	REV	36	A
GTRQARRNRK		10	HIV	REV	36	A
GTRQARRNRRK		11	HIV	REV	36	A
GTRQTRKNK		9	HIV	REV	37	A
GTRQTRKNRK		10	HIV	REV	37	A
GTRQTRKNRRK		11	HIV	REV	37	A
RVRRRRWRAR		10	HIV	REV	43	A
KVRRRRWRAR		10	HIV	REV	43	A
LTISYGRK		8	HIV	TAT	46	A
KTLGISYGR		9	HIV	TAT	44	A
LTISYGRKK		9	HIV	TAT	46	A
GTSYGRKKR		9	HIV	TAT	47	A
GTGISYGRK		9	HIV	TAT	45	A
KTLGISYGRK		10	HIV	TAT	44	A
LTISYGRKKR		10	HIV	TAT	46	A
KTLGISYGRKK		11	HIV	TAT	44	A
TVCNNCYCK		9	HIV	TAT	23	A
LVISYGRKKRR		11	HIV	TAT	46	A
ISYGRKKRRQK		11	HIV	TAT	48	A
ETGPSGQPCK		10	HIV	TAT	101	A
KVGPGGYPRR		10	HIV	TAT	101	A
KAGPGGYPRK		10	HIV	TAT	101	A
KVGPGGYPRRK		11	HIV	TAT	101	A
AVPGGYPRR		9	HIV	TAT	102	A
AVPGGYPRRK		10	HIV	TAT	102	A
KVGSLQYLK		9	HIV	VIF	146	A
ETVRHFPR		8	HIV	VPR	29	A
AACHKCIDFY		10	HPV	E6	63	
LLIRCLRCQK		10	HPV	E6	101	
KISEYRHYNY		10	HPV	E6	72	
AVCRVCLLFY		10	HPV	E6	64	
FAFTDLTIVY		10	HPV	E6	45	
FAFADLTVVY		10	HPV	E6	45	
RFLSKISEYR		10	HPV	E6	68	
ILIRCIICQR		10	HPV	E6	99	
RTAMFQDPQER		11	HPV	E6	5	

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
AMFQDPQERPR		11	HPV	E6	7	
MFQDPQERPRK		11	HPV	E6	8	
DLLIRCINCQK		11	HPV	E6	105	
RFEDPTRRPYK		11	HPV	E6	3	
ELTEVFEFAFK		11	HPV	E6	40	
GLYNLLIRCLR		11	HPV	E6	97	
NLLIRCLRCQK		11	HPV	E6	100	
EVLEESVHEIR		11	HPV	E6	17	
EVYKFLFTDLR		11	HPV	E6	41	
FLFTDLRIVYR		11	HPV	E6	45	
EVLEIPLIDLR		11	HPV	E6	20	
DLRLSCVYCKK		11	HPV	E6	28	
EVYNFACTELK		11	HPV	E6	44	
RVCLLFYSKVR		11	HPV	E6	67	
LLFYSKVRKYR		11	HPV	E6	70	
QLCDLLIRCYR		11	HPV	E6	98	
TLEQTVKK		8	HPV	E6	87	
ATRDLCIVYR		10	HPV	E6	53	A
AFRDLCIVYK		10	HPV	E6	53	A
ATCDKCLKFY		10	HPV	E6	68	A
AVCDKCLKFR		10	HPV	E6	68	A
KLYSKISEYR		10	HPV	E6	75	A
KFYSKISEYK		10	HPV	E6	75	A
KFSEYRHYCY		10	HPV	E6	79	A
KISEYRHYCR		10	HPV	E6	79	A
LFIRCINCQK		10	HPV	E6	106	A
LLIRCINCQR		10	HPV	E6	106	A
KVRFHNIRGR		10	HPV	E6	129	A
KQRFHNIRGK		10	HPV	E6	129	A
WFGRCMSCCR		10	HPV	E6	139	A
WTGRCMSCCK		10	HPV	E6	139	A
MTCCRSSRTR		10	HPV	E6	144	A
MSCCRSSRTK		10	HPV	E6	144	A
STCRSSRTRR		10	HPV	E6	145	A
SCCRSSRTRK		10	HPV	E6	145	A
DIEITCVYCR		10	HPV	E6	27	A
FTFKDLFVVY		10	HPV	E6	47	A
FAFKDLFVVK		10	HPV	E6	47	A
AVKDLFVVYR		10	HPV	E6	48	A
AFKDLFVVYK		10	HPV	E6	48	A
FVVYRDSIPK		10	HPV	E6	53	A
DTIPHAACHK		10	HPV	E6	58	A
DSIPHAACHR		10	HPV	E6	58	A
KFIDFYSRIR		10	HPV	E6	67	A
DTVYGDTLEK		10	HPV	E6	83	A
DSVYGDTLER		10	HPV	E6	83	A
LFIRCLRCQK		10	HPV	E6	101	A
LLIRCLRCQR		10	HPV	E6	101	A
RVHNIAGHYR		10	HPV	E6	126	A

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
RFHNIAGHYK		10	HPV	E6	126	A
RTQCHSCCNR		10	HPV	E6	135	A
RGQCHSCCNK		10	HPV	E6	135	A
ATTDLTIVYR		10	HPV	E6	46	A
AFTDLTIVYK		10	HPV	E6	46	A
RLYSKVSEFR		10	HPV	E6	68	A
RFYSKVSEFK		10	HPV	E6	68	A
KFSEFRWYRY		10	HPV	E6	72	A
KVSEFRWYRR		10	HPV	E6	72	A
YFVYGTTLEK		10	HPV	E6	81	A
YSVYGTTLER		10	HPV	E6	81	A
GTTLEKLTNR		10	HPV	E6	85	A
LVIRCITCQR		10	HPV	E6	99	A
LLIRCITCQK		10	HPV	E6	99	A
WVGRCIACWR		10	HPV	E6	132	A
WTGRCIACWK		10	HPV	E6	132	A
RTIACWRRPR		10	HPV	E6	135	A
RCIACWRRPK		10	HPV	E6	135	A
AVADLTVVYR		10	HPV	E6	46	A
AFADLTVVYK		10	HPV	E6	46	A
RVLSKISEYR		10	HPV	E6	68	A
RFLSKISEYK		10	HPV	E6	68	A
KFSEYRHYNY		10	HPV	E6	72	A
KISEYRHYNR		10	HPV	E6	72	A
ITIRCIICQR		10	HPV	E6	99	A
ILIRCIICQK		10	HPV	E6	99	A
WVGRCAACWR		10	HPV	E6	132	A
WAGRCAACWK		10	HPV	E6	132	A
CFACWRSRRR		10	HPV	E6	136	A
DTSIACVYCK		10	HPV	E6	27	A
DVSIACVYCR		10	HPV	E6	27	A
CVYCKATLEK		10	HPV	E6	32	A
RFEVYQFAFK		10	HPV	E6	41	A
RTEVYQFAFR		10	HPV	E6	41	A
AVKDLCIVYR		10	HPV	E6	48	A
AFKDLCIVYK		10	HPV	E6	48	A
ATCHKCIDFY		10	HPV	E6	63	A
AACHKCIDFK		10	HPV	E6	63	A
NLVYGETLEK		10	HPV	E6	83	A
NSVYGETLER		10	HPV	E6	83	A
LSIRCLRCQK		10	HPV	E6	101	A
LLIRCLRCQY		10	HPV	E6	101	A
RVHSIAGQYR		10	HPV	E6	126	A
RFHSIAGQYK		10	HPV	E6	126	A
LVTDLRIVYR		10	HPV	E6	46	A
LFTDLRIVYK		10	HPV	E6	46	A
CTMCLRFLSK		10	HPV	E6	63	A
CIMCLRFLSR		10	HPV	E6	63	A
RLLSKISEYR		10	HPV	E6	68	A

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
RFLSKISEYY		10	HPV	E6	68	A
SFYGKTLEER		10	HPV	E6	82	A
SLYGKTLEEK		10	HPV	E6	82	A
WFGRCSECWR		10	HPV	E6	132	A
WTGRCSECWK		10	HPV	E6	132	A
AFCRVCLLFY		10	HPV	E6	64	A
AVCRVCLLFR		10	HPV	E6	64	A
CFLFYSKVRK		10	HPV	E6	69	A
CLLFYSKVRR		10	HPV	E6	69	A
LVYSKVRKYR		10	HPV	E6	71	A
LFYSKVRKYK		10	HPV	E6	71	A
GTTLESITKK		10	HPV	E6	88	A
WVGSCLGCWR		10	HPV	E6	135	A
WTGSCLGCWK		10	HPV	E6	135	A
VVADLRIVYR		10	HPV	E6	46	A
VFADLRIVYK		10	HPV	E6	46	A
RTLSKISEYR		10	HPV	E6	68	A
RLLSKISEYK		10	HPV	E6	68	A
KVSEYRHYNY		10	HPV	E6	72	A
KISEYRHYNK		10	HPV	E6	72	A
IVIRCIICQR		10	HPV	E6	99	A
WLGRCAVCWR		10	HPV	E6	132	A
WTGRCAVCWK		10	HPV	E6	132	A
YVVCDKCLK		9	HPV	E6	67	A
YAVCDKCLR		9	HPV	E6	67	A
SVCRSSRTR		9	HPV	E6	145	A
SCCRSSRTK		9	HPV	E6	145	A
SLPHAACHK		9	HPV	E6	59	A
SIPHAACHR		9	HPV	E6	59	A
FVDLTIVYR		9	HPV	E6	47	A
FTDLTIVYK		9	HPV	E6	47	A
SFYGTTLEK		9	HPV	E6	82	A
SVYGTTLER		9	HPV	E6	82	A
TFLEKLTNK		9	HPV	E6	86	A
TTLEKLTNR		9	HPV	E6	86	A
ETNPFGICK		9	HPV	E6	56	A
EGNPFGICR		9	HPV	E6	56	A
NTLEQTVKR		9	HPV	E6	86	A
ALCWRSRRR		9	HPV	E6	137	A
AACWRSRRK		9	HPV	E6	137	A
VSIACVYCR		9	HPV	E6	28	A
SIACVYCKK		9	HPV	E6	29	A
ILYRDCIAY		9	HPV	E6	54	A
IVYRDCIAR		9	HPV	E6	54	A
CTAYAACHK		9	HPV	E6	59	A
CIAYAACHR		9	HPV	E6	59	A
SFYGETLEK		9	HPV	E6	84	A
SVYGETLER		9	HPV	E6	84	A
LIRCLRCQR		9	HPV	E6	102	A

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
RTQCVQCKK		9	HPV	E6	27	A
RLQCVQCKR		9	HPV	E6	27	A
KFLEERVKK		9	HPV	E6	86	A
KTLEERVKR		9	HPV	E6	86	A
NVMGRWTGR		9	HPV	E6	127	A
NIMGRWTGK		9	HPV	E6	127	A
LTYRDDFPY		9	HPV	E6	55	A
LVYRDDFPK		9	HPV	E6	55	A
RFCLLFYSK		9	HPV	E6	67	A
RVCLLFYSR		9	HPV	E6	67	A
LTFYSKVRK		9	HPV	E6	70	A
LLFYSKVRR		9	HPV	E6	70	A
ATLESITKR		9	HPV	E6	89	A
KVLCDLLIR		9	HPV	E6	97	A
KQLCDLLIK		9	HPV	E6	97	A
TFVHEIELK		9	HPV	E6	21	A
TSVHEIELR		9	HPV	E6	21	A
YTFVFADLR		9	HPV	E6	43	A
DFLEQTLKK		9	HPV	E6	86	A
DTLEQTLKR		9	HPV	E6	86	A
LVRCIICQR		9	HPV	E6	100	A
LIRCIICQK		9	HPV	E6	100	A
RVAVCWRPR		9	HPV	E6	135	A
RCAVCWRPK		9	HPV	E6	135	A
AFCWRPRRR		9	HPV	E6	137	A
AVCWRPRRK		9	HPV	E6	137	A
LSFVCPWCA		9	HPV	E7	94	
TFCCKCDSTLR		11	HPV	E7	56	
LVVESSADDLR		11	HPV	E7	74	
TLQVVCPGCAR		11	HPV	E7	88	
YLIHVPCCECK		11	HPV	E7	59	
FVVQLDIQSTK		11	HPV	E7	70	
HTCNTTVR		8	HPV	E7	59	
GLVCPICSQK		10	HPV	E7	88	A
GFNHQHLPAR		10	HPV	E7	43	A
GVNHQHLPAK		10	HPV	E7	43	A
NVVTFCCQCK		10	HPV	E7	53	A
NIVTFCCQCR		10	HPV	E7	53	A
GVSHAQLPAK		10	HPV	E7	44	A
LIHVPCCECR		10	HPV	E7	60	A
AVLQDIVLH		9	HPV	E7	6	A
ATLQDIVLK		9	HPV	E7	6	A
GVNHQHLPK		9	HPV	E7	43	A
HVMLCMCCK		9	HPV	E7	59	A
HTMLCMCCR		9	HPV	E7	59	A
LSFVCPWCR		9	HPV	E7	94	A
AQPATADYK		9	HPV	E7	45	A
VVHAQLPAR		9	HPV	E7	45	A
VSHAQLPAK		9	HPV	E7	45	A

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
QLARQAKQH		9	HPV	E7	48	A
KQHTCYLIR		9	HPV	E7	54	A
VTLDIQSTK		9	HPV	E7	72	A
VQLDIQSTR		9	HPV	E7	72	A
SLGPGPGTK		9	Human	MAGE1	96	A
SLFGPGPGK		9	Human	MAGE1	96	A
LVGPGPGK		8	Human	MAGE2	116	A
KMFLQLAK		8	Human	p53	132	
KMGPGPGK		8	Human	p53	132	A
KQENWYSLKK		10	Pf	CSP	58	
GVGPGPGLK		9	Pf	LSA1	105	A
GVSGPGPGK		9	Pf	LSA1	105	A
FLLYILFLVK		10	Pf		17	
LVFSNVLCFR		10	Pf		43	
SSFDIKSEVK		10	Pf		116	
TLYQIQVMKR		10	Pf		44	
KQVQMMIMIK		10	Pf		58	
GVIYIMIISK		10	Pf		70	
ELFDKDTFFK		10	Pf		158	
ALERLLSLKK		10	Pf		50	
KILIKIPVTK		10	Pf		109	
RLPLLPKTWK		10	Pf		128	
SQVSNSDSYK		10	Pf		161	
QQNQESKIMK		10	Pf		197	
IIALLIIPPK		10	Pf		249	
SSPLFNNFYK		10	Pf		14	
FLYLLNKKNK		10	Pf		151	
LQMMNVNLQK		10	Pf		183	
LTNHLINTPK		10	Pf		195	
IFISFYLINK		10	Pf		259	
RLFEESLGIR		10	Pf		293	
LLYILFLVK		9	Pf		18	
KSMLKELIK		9	Pf		129	
PVLTSLFNK		9	Pf		166	
KTMNNYMIK		9	Pf		18	
LFDKDTFFK		9	Pf		159	
YLFNQHIKK		9	Pf		287	
MQSSFFMNR		9	Pf		307	
RFYITTRYK		9	Pf		315	
TTRYKYLNK		9	Pf		319	
AVIFTPIYY		9	Pf		34	
ALERLLSLK		9	Pf		50	
SISGKYDIK		9	Pf		85	
EQRLPLLPK		9	Pf		126	
IALLIIPPK		9	Pf		250	
PVVCSMEYK		9	Pf		270	
VVCSMEYKK		9	Pf		271	
FSYDLRLNK		9	Pf		308	
HLNIPIGFK		9	Pf		323	

HLA-A3 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
PLFNNFYKR		9	Pf		16	
YQNFQNADK		9	Pf		141	
QMMNVNLQK		9	Pf		184	
AVSEIQNNK		9	Pf		222	
GTMYILLKK		9	Pf		236	
FISFYLINK		9	Pf		260	
YLINKHWQR		9	Pf		264	
ALKISQLQK		9	Pf		273	
KINSNFLLK		9	Pf		282	
AAMXDPTTFK		10	Unknown	Naturally processed		A
GTMTTSXYK		9	Unknown	Naturally processed		A
SXXPAXFQK		9	Unknown	Naturally processed		A
ATAGDGXXEXRK		12	Unknown	Naturally processed		A

TABLE 16

HLA-A3 SUPERTYPE					
Sequence	**A*0301**	**A*1101**	**A*3101**	**A*3301**	**A*6801**
ALNAAAAAK	74	21	10954	>72500	80000
ALAAGAAAK	19	37			
ALQAAAAAK	57	65	51962	>72500	>80000
STGPGPGVVRR	18695	367	95	5983	5.8
STLGPGPGVRR	892	19	42	670	3.8
STLPGPGPGRR	297	19	61	1893	25
STLPEGPGPGR	325	26	28	822	30
QAGFFLLTR	10138	1678	302	182	5.3
RVHFASPLH	12	60	572	>122881.36	7620
AAYAAQGYK	18	18	1175	14074	34
KSKFGYGAK	36	596	116	>122881.36	>7626.31
PAAYAAQGYK	950	456	20314	>110687.02	666
RMYVGGVEH	3.8	274	162	>122881.36	>28776.98
SQLSAPSLK	306	25	1276	>122881.36	3845
TSCGNTLTCY	>36666.67	5.0			
VTGPGPGPVWK	2900	24	12964	>102836.88	425
VTVGPGPGVWK	174	2.7	2731	75360	21
VTVYGPGPGWK	1151	18	>8995.5	>102836.88	206
VTVYYGPGPGK	310	24	9720	101830	30
PVRPQVPLR	>10901.88	16112	332	3439	7012
HGAITSSNTK	2837	344	>16143.5	>22924.9	1235
AVDLSFFLK	226	23	6207	>27831.09	4038
DVSHFLKEK	>9298.39	5645	>17839.44	232	135
GVLDGLIYSK	1080	21	6007	>25151.78	831
GVDGLIYSK	10089	47	>17664.38	>29652.35	5100
EILDLWVYK	1032	64	>5774.78	288	93
ILDLWVYK	1265	320	13680	30096	12092
RVPLTFGWCFK	69	30	102	26651	571
QVYTPGPGTR	1249	852	1764	3334	273
AVGPGPGLK	18	3.6	128	75754	444
AVDGPGPGK	179	19	36837	>112403.1	2132
QMGPGPGNFK	49	22	2682	100771	63
QMAGPGPGFK	9.4	6.2	667	4784	30
QMAVGPGPGK	33	16	5961	86676	22
TVGPGPGPEK	115	17	10140	98177	23
TVQGPGPGEK	218	3.4	9874	103379	195
TVQPGPGPGK	41	2.5	1335	68584	28
VAIKIGGQLK	2593	151	46875	51222	123
VTVKIGGQLK	296	61	24385	104757	147
VTIKVGGQLK	188	59	6061	47647	127
VTIRIGGQLK	51	14	4458	65764	25
VTVRIGGQLK	226	15	5380	40344	49
VTVKVGGQLK	206	54	21484	46182	104
VTIRVGGQLK	43	13	3591	86086	28
VTVRVGGQLK	216	19	8238	>72319.2	141
VTVKIGGQLR	19185	194	417	3833	52
VTIRIGGQLR	3192	23	61	1352	16

HLA-A3 SUPERTYPE

Sequence	A*0301	A*1101	A*3101	A*3301	A*6801
VTIKLGGQIR	43252	219	590	12965	104
VSIKVGGQIK	1921	86	57069	>72319.2	2026
VSIRVGGQIK	642	91	50677	>61702.13	1960
VTVKIEGQLK	647	23	4616	64604	30
VTIKIEGQLK	361	69	5077	58024	27
VTVKIEGQLR	35612	143	394	4057	146
VSIRVGGQTK	341	21	29949	38958	290
VSIRVGGQTR	18531	241	466	8595	288
VTVRIGGMQK	54	13	2583	44425	155
ITVKIGKEVR	>69182.39	12904	5057	24985	154
GTRQARRNK	67	749	9713	45966	59708
GTRQARRNRK	100	634	3800	>42335.77	7788
GTRQARRNRRK	404	2596	7774	>24308.47	9104
GTRQTRKNK	198	3104	13373	>29713.11	18657
GTRQTRKNRK	129	1082	2485	60183	5998
GTRQTRKNRRK	478	4184	4008	>24308.47	>17167.38
RVRRRRWRAR	2443	>16759.78	265	3758	>36866.36
KVRRRRWRAR	327	>20905.92	342	3243	15501
LTISYGRK	988	708	27068	38162	482
KTLGISYGR	53	9.8	21	502	36
LTISYGRKK	584	69	13918	59654	63
GTSYGRKKR	9965	5916	225	21588	5778
GTGISYGRK	480	77	58102	>43740.57	7407
KTLGISYGRK	36	79	841	42378	1629
LTISYGRKKR	7161	1229	71	2515	33
KTLGISYGRKK	52	285	91	23401	647
TVCNNCYCK	9920	267	8793	28481	876
LVISYGRKKRR	>11702.13	8669	562	267	4662
ISYGRKKRRQK	48	2807	3147	>20000	4428
ETGPSGQPCK	>14569.54	3501	>22500	>17813.27	50
KVGPGGYPRR	2268	487	250	7904	721
KAGPGGYPRK	62	43	10734	>17813.27	5555
KVGPGGYPRRK	70	87	775	>5063.73	921
AVPGGYPRR	3012	1215	1349	3453	109
AVPGGYPRRK	819	60	39974	>5570.5	846
KVGSLQYLK	482	70	2104	>43740.57	4200
ETVRHFPR	>13513.51	4183	1000	81	86
AACHKCIDFY	18824	261	20643	>116465.86	32548
LLIRCLRCQK	437	170	6612	28936	78
KISEYRHYNY	42	112	1426	35341	25077
AVCRVCLLFY	77	21	1978	4520	1302
FAFTDLTIVY	40343	21161	42065	131202	346
FAFADLTVVY	18592	5866	23676	26768	402
RFLSKISEYR	1640	18468	33	436	172
ILIRCIICQR	8550	5012	377	2480	537
RTAMFQDPQER	1478	103	49	3459	19
AMFQDPQERPR	1718	886	45	1787	1478
MFQDPQERPRK	15493	8571	604	419	16729
DLLIRCINCQK	2923	935	4884	29	263

HLA-A3 SUPERTYPE

Sequence	A*0301	A*1101	A*3101	A*3301	A*6801
RFEDPTRRPYK	169	432	53	1758	7338
ELTEVFEFAFK	8966	582	25205	1733	15
GLYNLLIRCLR	1268	1568	250	401	1624
NLLIRCLRCQK	1565	854	3140	397	1480
EVLEESVHEIR	>45643.15	>20202.02	31037	212	240
EVYKFLFTDLR	31240	602	759	4.3	11
FLFTDLRIVYR	672	227	58	21	1.4
EVLEIPLIDLR	>47008.55	16638	36427	72	27
DLRLSCVYCKK	3644	1907	17023	109	3002
EVYNFACTELK	1622	117	484	5.9	2.7
RVCLLFYSKVR	771	190	221	1061	1267
LLFYSKVRKYR	28	94	7.0	11	15
QLCDLLIRCYR	1240	700	450	106	489
TLEQTVKK	4766	203	>100000	>75324.68	21400
ATRDLCIVYR	237	156	4.7	44	28
AFRDLCIVYK	31	15	10	132	57
ATCDKCLKFY	194	17	491	18080	4562
AVCDKCLKFR	77	15	11	45	34
KLYSKISEYR	5.4	168	6.4	28	91
KFYSKISEYK	7.6	674	27	329	208
KFSEYRHYCY	5092	7485	308	49397	14571
KISEYRHYCR	486	688	25	833	1488
LFIRCINCQK	2880	702	52	42	56
LLIRCINCQR	2818	686	30	50	14
KVRFHNIRGR	39	8632	27	4500	3979
KQRFHNIRGK	55	1953	573	35208	22879
WFGRCMSCCR	16071	10690	288	98	303
WTGRCMSCCK	6687	841	6496	15191	118
MTCCRSSRTR	3825	933	410	601	2.2
MSCCRSSRTK	352	169	2333	6916	12
STCRSSRTRR	2989	118	152	1020	312
SCCRSSRTRK	326	3272	5592	20916	8777
DIEITCVYCR	2014	826	3780	448	422
FTFKDLFVVY	14364	1208	10757	2725	62
FAFKDLFVVK	783	71	525	1066	3.6
AVKDLFVVYR	1728	91	3.1	9.1	3.3
AFKDLFVVYK	3256	211	32	93	576
FVVYRDSIPK	265	81	6216	146	30
DTIPHAACHK	2366	701	1763	9.3	23
DSIPHAACHR	2772	853	357	2.2	27
KFIDFYSRIR	8891	9008	3.3	677	2551
DTVYGDTLEK	50	15	28754	55090	31
DSVYGDTLER	292	23	485	891	28
LFIRCLRCQK	3390	1533	218	77	200
LLIRCLRCQR	3360	1396	28	75	13
RVHNIAGHYR	30	21	22	114	18
RFHNIAGHYK	25	22	2.6	80	23
RTQCHSCCNR	338	20	22	132	161
RGQCHSCCNK	6135	113	425	37669	20340

HLA-A3 SUPERTYPE					
Sequence	**A*0301**	**A*1101**	**A*3101**	**A*3301**	**A*6801**
ATTDLTIVYR	247	10	34	1739	14
AFTDLTIVYK	701	112	3952	9380	215
RLYSKVSEFR	6.4	131	24	690	73
RFYSKVSEFK	27	521	30	4452	547
KFSEFRWYRY	4750	1595	34	856	12811
KVSEFRWYRR	266	16	2.8	159	30
YFVYGTTLEK	204	62	2167	15740	53
YSVYGTTLER	430	96	2136	6903	19
GTTLEKLTNR	3604	1720	382	706	2946
LVIRCITCQR	2222	255	54	135	14
LLIRCITCQK	291	120	3009	2165	40
WVGRCIACWR	6227	1391	85	13	9.7
WTGRCIACWK	2633	55	3078	169	24
RTIACWRRPR	40	63	3.2	95	51
RCIACWRRPK	1535	1476	292	176	1655
AVADLTVVYR	489	11	31	892	7.3
AFADLTVVYK	2365	107	1113	13557	50
RVLSKISEYR	34	84	24	197	136
RFLSKISEYK	31	287	42	10237	112
KFSEYRHYNY	5819	5521	286	18351	1798
KISEYRHYNR	58	140	17	161	1579
ITIRCIICQR	488	93	50	123	12
ILIRCIICQK	192	78	1383	1423	165
WVGRCAACWR	2757	3973	360	24	19
WAGRCAACWK	4662	583	23311	1491	50
CFACWRSRRR	23542	7164	578	165	10206
DTSIACVYCK	2936	89	5385	1968	216
DVSIACVYCR	2814	217	406	487	658
CVYCKATLEK	418	653	5307	17928	862
RFEVYQFAFK	38	611	179	2867	2443
RTEVYQFAFR	217	78	12	142	147
AVKDLCIVYR	841	66	7.3	8.0	6.5
AFKDLCIVYK	856	47	39	263	378
ATCHKCIDFY	133	7.4	1164	12691	1386
AACHKCIDFK	118	20	437	53733	414
NLVYGETLEK	846	143	761	121	87
NSVYGETLER	150	25	163	1333	18
LSIRCLRCQK	245	14	100	1135	17
LLIRCLRCQY	727	452	2894	2430	254
RVHSIAGQYR	31	34	7.6	812	28
RFHSIAGQYK	17	43	1.3	629	83
LVTDLRIVYR	3869	648	20	150	6.8
LFTDLRIVYK	628	263	258	149	277
CTMCLRFLSK	1002	226	6274	3945	429
CIMCLRFLSR	41	101	167	83	155
RLLSKISEYR	5.2	662	7.7	108	21
RFLSKISEYY	1702	25535	14	41096	3999
SFYGKTLEER	642	205	17	66	42
SLYGKTLEEK	7.9	6.8	1044	6516	29

HLA-A3 SUPERTYPE

Sequence	A*0301	A*1101	A*3101	A*3301	A*6801
WFGRCSECWR	1788	1569	20	5.5	26
WTGRCSECWK	2492	26	3323	720	22
AFCRVCLLFY	509	272	1777	1202	173
AVCRVCLLFR	20	1.8	2.1	64	21
CFLFYSKVRK	125	96	81	315	172
CLLFYSKVRR	417	204	159	386	242
LVYSKVRKYR	320	619	17	49	31
LFYSKVRKYK	680	2582	18	30	1976
GTTLESITKK	622	108	85182	132509	10147
WVGSCLGCWR	48682	5520	20	15	9.3
WTGSCLGCWK	7705	6.9	18344	2980	3.7
VVADLRIVYR	513	18	41	101	16
VFADLRIVYK	2086	127	402	200	273
RTLSKISEYR	77	100	52	189	133
RLLSKISEYK	15	65	158	40019	429
KVSEYRHYNY	349	110	1791	70859	3498
KISEYRHYNK	29	18	397	24827	15565
IVIRCIICQR	984	217	52	529	28
WLGRCAVCWR	2330	3002	356	40	112
WTGRCAVCWK	1261	131	4176	3403	29
YVVCDKCLK	3282	643	8.5	165	1289
YAVCDKCLR	458	194	4261	26582	16034
SVCRSSRTR	323	97	249	547	17
SCCRSSRTK	21	3.9	51	5227	4.2
SLPHAACHK	32	66	219	1186	654
SIPHAACHR	1053	352	236	253	181
FVDLTIVYR	29674	5312	2384	430	138
FTDLTIVYK	557	16	24170	18477	143
SFYGTTLEK	34	15	517	3385	498
SVYGTTLER	28	6.4	133	454	21
TFLEKLTNK	6839	815	451	148	918
TTLEKLTNR	1993	817	42	37	101
ETNPFGICK	9585	100	29103	804	14
EGNPFGICR	11467	10372	5123	344	82
NTLEQTVKR	20380	1151	2273	18	8.6
ALCWRSRRR	959	9748	72	1289	7416
AACWRSRRK	75	770	3022	45341	12877
VSIACVYCR	3236	143	42	1347	185
SIACVYCKK	271	83	9114	19632	96
ILYRDCIAY	261	1832	53232	44670	>19607.84
IVYRDCIAR	465	106	27	325	64
CTAYAACHK	726	196	2956	771	167
CIAYAACHR	3625	1905	502	115	262
SFYGETLEK	288	108	947	885	1074
SVYGETLER	44	11	235	160	17
LIRCLRCQR	21335	12648	695	810	200
RTQCVQCKK	234	20	127	8147	3066
RLQCVQCKR	2535	6081	65	1829	11479
KFLEERVKK	5344	2229	30	9740	17674

HLA-A3 SUPERTYPE

Sequence	A*0301	A*1101	A*3101	A*3301	A*6801
KTLEERVKR	1957	159	37	1360	17685
NVMGRWTGR	3884	794	40	18	20
NIMGRWTGK	52	54	3274	86	173
LTYRDDFPY	8265	82	>71146.25	20186	1529
LVYRDDFPK	317	13	3009	1970	130
RFCLLFYSK	1156	484	83	450	232
RVCLLFYSR	439	111	51	2176	689
LTFYSKVRK	3.8	8.0	87	3382	13
LLFYSKVRR	56	73	38	276	11
ATLESITKR	1437	16	100	851	188
KVLCDLLIR	363	169	66	5896	9053
KQLCDLLIK	226	65	340	46426	11897
TFVHEIELK	4431	217	8412	4130	172
TSVHEIELR	>64327.49	872	1039	5948	12
YTFVFADLR	3633	8.1	20	6.6	2.9
DFLEQTLKK	>57591.62	18809	34365	174	14376
DTLEQTLKR	31347	12909	38127	9.2	110
LVRCIICQR	677	358	59	109	201
LIRCIICQK	445	252	639	834	285
RVAVCWRPR	5.3	8.5	7.0	102	33
RCAVCWRPK	285	340	382	131	1297
AFCWRPRRR	273	17907	60	75	1087
AVCWRPRRK	34	101	263	7950	1810
LSFVCPWCA	38337	10864	4289	4603	341
TFCCKCDSTLR	21772	8043	332	91	260
LVVESSADDLR	>47008.55	2170	26410	5624	28
TLQVVCPGCAR	20997	1395	67	63	147
YLIHVPCCECK	1748	1534	33044	8066	177
FVVQLDIQSTK	3682	853	48593	31350	2.7
HTCNTTVR	4862	1792	726	4490	25
GLVCPICSQK	428	814	45293	70317	3568
GFNHQHLPAR	>46610.17	27889	173	5572	34617
GVNHQHLPAK	42	11	3337	76239	9347
NVVTFCCQCK	790	303	4757	87	13
NIVTFCCQCR	1507	1070	2731	766	93
GVSHAQLPAK	42	12	36011	>74935.4	20590
LIHVPCCECR	5326	5925	385	387	228
AVLQDIVLH	1922	101	6307	25776	27035
ATLQDIVLK	37	8.6	65	17121	3231
GVNHQHLPK	26	7.7	353	15615	1192
HVMLCMCCK	282	79	772	825	99
HTMLCMCCR	405	92	11	14	24
LSFVCPWCR	31676	200	47	231	152
AQPATADYK	3500	109	10413	58871	24173
VVHAQLPAR	423	127	3.4	12	201
VSHAQLPAK	378	9.5	46	1401	13502
QLARQAKQH	8423	6862	945	1665	243
KQHTCYLIR	135	213	13	2275	12177
VTLDIQSTK	78	13	2046	1954	237

HLA-A3 SUPERTYPE

Sequence	A*0301	A*1101	A*3101	A*3301	A*6801
VQLDIQSTR	15105	2917	162	4588	10341
SLGPGPGTK	7.8	5.8	4392	152133	3517
SLFGPGPGK	3.4	2.3	1085	82275	36
LVGPGPGK	1004	291	23907	>125541.13	598
KMFLQLAK	45	62	677	>125541.13	8384
KMGPGPGK	84	242	1144	106362	4156
KQENWYSLKK	608	178	6327	>136150.23	4794
GVGPGPGLK	47	4.0	1367	>111538.46	3972
GVSGPGPGK	13	5.8	>11221.95	>111538.46	209
FLLYILFLVK	446	1431	54496	3254	2266
LVFSNVLCFR	120	19	33	19	7.7
SSFDIKSEVK	1900	19	19829	70344	31
TLYQIQVMKR	361	164	397	558	90
KQVQMMIMIK	264	112	4627	1231	2247
GVIYIMIISK	777	18	18811	1567	1134
ELFDKDTFFK	144	109	3676	13	3.6
ALERLLSLKK	147	822	33559	18255	22391
KILIKIPVTK	13	60	1661	24992	19571
RLPLLPKTWK	11	67	340	11392	2889
SQVSNSDSYK	1656	83	24559	>17448.86	1384
QQNQESKIMK	3469	77	28120	>17448.86	21310
IIALLIIPPK	30	5.3	23822	8426	82
SSPLFNNFYK	100	0.7	1608	1728	6.3
FLYLLNKKNK	177	475	4313	780	155
LQMMNVNLQK	25	7.2	435	1113	320
LTNHLINTPK	11	5.9	62	373	10
IFISFYLINK	1987	1056	462	394	363
RLFEESLGIR	64	1096	297	788	409
LLYILFLVK	13	207	90687	13261	5545
KSMLKELIK	189	151	450	>46548.96	>37037.04
PVLTSLFNK	1949	25	5107	18271	29928
KTMNNYMIK	17	5.5	24	12743	29
LFDKDTFFK	931	167	5706	1189	101
YLFNQHIKK	14	7.8	4919	7974	14
MQSSFFMNR	13	1.1	29	75	3.8
RFYITTRYK	1.9	67	15	98	17468
TTRYKYLNK	117	848	416	652	2565
AVIFTPIYY	25	9.5	42321	10068	1352
ALERLLSLK	233	369	3433	12786	13708
SISGKYDIK	2086	50	28249	12437	1745
EQRLPLLPK	1088	765	423	987	1911
IALLIIPPK	1241	108	2926	1404	1965
PVVCSMEYK	1940	80	330791	22608	414
VVCSMEYKK	443	54	891	14328	167
FSYDLRLNK	29	4.9	461	1264	15
HLNIPIGFK	2.3	1.3	183	97	2.8
PLFNNFYKR	2635	1890	520	1258	132
YQNFQNADK	2712	177	44698	>18447.84	19830
QMMNVNLQK	20	7.0	504	6649	243

HLA-A3 SUPERTYPE					
Sequence	**A*0301**	**A*1101**	**A*3101**	**A*3301**	**A*6801**
AVSEIQNNK	25	11	1429	25449	14
GTMYILLKK	2.2	1.2	29	8453	3.1
FISFYLINK	19	9.0	2192	1456	18
YLINKHWQR	1034	676	4.4	7.7	3.7
ALKISQLQK	15	96	3203	23800	>54794.52
KINSNFLLK	17	6.4	68	47740	2737
AAMXDPTTFK	50	7.2			
GTMTTSXYK	4.0	4.5			
SXXPAXFQK	14	2.0			
ATAGDGXXEXRK	184	19			

TABLE 17

HLA-A24 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
AYGPGPGKF		9	Artificial sequence	Consensus		A
AYIGPGPGF		9	Artificial sequence	Consensus		A
AYAAAAAAL		9	Artificial sequence			Poly
AYSSWMYSY		9	EBV	EBNA3	176	
DLLDTASALY		10	HBV	Core	419	
WFHISCLTF		9	HBV	NUC	102	
KYTSFPWL		8	HBV	pol	745	
FAAPFTQCGY		10	HBV	pol	631	
SYQHFRKLLL		10	HBV	POL	4	
LYSHPIILGF		10	HBV	POL	492	
MSTTDLEAY		9	HBV	X	103	
MYVGDLCGSVF		11	HCV	E1	275	
MYGPGPGGSVF		11	HCV	E1	275	A
MYVGPGPGSVF		11	HCV	E1	275	A
MYVGGPGPGVF		11	HCV	E1	275	A
MYVGDGPGPGF		11	HCV	E1	275	A
VMGSSYGF		8	HCV	NS5	2639	
EVDGVRLHRY		10	HCV	NS5	2129	
KYSKSSIVGW		10	HIV	NEF	4	A
KWSKSSIVGF		10	HIV	NEF	4	A
FFLKEKGGF		9	HIV	NEF	116	A
IYSKKRQEF		9	HIV	NEF	175	A
IYSKKRQEIF		10	HIV	NEF	175	A
LYVYHTQGYF		10	HIV	NEF	190	A
VYHTQGYFPDF		11	HIV	NEF	192	A
RYPLTFGW		8	HIV	NEF	216	
RYPLTFGF		8	HIV	NEF	216	A
RFPLTFGF		8	HIV	NEF	216	A
TYGWCFKL		8	HIV	NEF	222	A
TFGWCFKF		8	HIV	NEF	222	A
LYVYHTQGY		9	HIV	NEF	190	A
NYTPGPGIRF		10	HIV	NEF	206	A
QYPPLERLTL		10	HIV	REV	78	A
QLPPLERLTF		10	HIV	REV	78	A
KYGSLQYLAL		10	HIV	VIF	146	A
LSKISEYRHY		10	HPV	E6	70	
ISEYRHYNY		9	HPV	E6	73	
RFHNIRGRW		9	HPV	E6	131	
RFLSKISEY		9	HPV	E6	68	
RFHNISGRW		9	HPV	E6	124	
VYDFAFRDLCI		11	HPV	E6	49	
PYAVCDKCLKF		11	HPV	E6	66	
QYNKPLCDLLI		11	HPV	E6	98	

HLA-A24 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
PFGICKLCLRF		11	HPV	E6	59	
VYQFAFKDLCI		11	HPV	E6	44	
AYAACHKCIDF		11	HPV	E6	61	
VYKFLFTDLRI		11	HPV	E6	42	
PYGVCIMCLRF		11	HPV	E6	59	
PYAVCRVCLLF		11	HPV	E6	62	
VYDFVFADLRI		11	HPV	E6	42	
QYNKPLCDLF		10	HPV	E6	98	A
VYEFAFKDLF		10	HPV	E6	44	A
FYSKVSEFRF		10	HPV	E6	69	A
VYREGNPFGF		10	HPV	E6	53	A
FYSRIRELRF		10	HPV	E6	71	A
PYAVCRVCLF		10	HPV	E6	62	A
FYSKVRKYRF		10	HPV	E6	72	A
LYGDTLEQTF		10	HPV	E6	83	A
VYDFAFRDF		9	HPV	E6	49	A
AYRDLCIVY		9	HPV	E6	53	A
AFRDLCIVF		9	HPV	E6	53	A
PYAVCDKCF		9	HPV	E6	66	A
KYYSKISEY		9	HPV	E6	75	A
KFYSKISEF		9	HPV	E6	75	A
CYSLYGTTF		9	HPV	E6	87	A
RYHNIRGRW		9	HPV	E6	131	A
RFHNIRGRF		9	HPV	E6	131	A
VYCKTVLEF		9	HPV	E6	33	A
AYKDLFVVY		9	HPV	E6	48	A
AFKDLFVVF		9	HPV	E6	48	A
LYVVYRDSI		9	HPV	E6	52	A
LFVVYRDSF		9	HPV	E6	52	A
RYHNIAGHY		9	HPV	E6	126	A
RFHNIAGHF		9	HPV	E6	126	A
VYGTTLEKF		9	HPV	E6	83	A
AYADLTVVY		9	HPV	E6	46	A
AFADLTVVF		9	HPV	E6	46	A
RYLSKISEY		9	HPV	E6	68	A
NYSVYGNTF		9	HPV	E6	80	A
RYHNISGRW		9	HPV	E6	124	A
AYKDLCIVY		9	HPV	E6	48	A
AFKDLCIVF		9	HPV	E6	48	A
AYAACHKCF		9	HPV	E6	61	A
VYGETLEKF		9	HPV	E6	85	A
RYHSIAGQY		9	HPV	E6	126	A
RFHSIAGQF		9	HPV	E6	126	A
KYLFTDLRI		9	HPV	E6	44	A
KFLFTDLRF		9	HPV	E6	44	A
LYTDLRIVY		9	HPV	E6	46	A
LFTDLRIVF		9	HPV	E6	46	A

HLA-A24 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
PYGVCIMCF		9	HPV	E6	59	A
RFLSKISEF		9	HPV	E6	68	A
EYRHYQYSF		9	HPV	E6	75	A
RYHNIMGRW		9	HPV	E6	124	A
RFHNIMGRF		9	HPV	E6	124	A
VYNFACTEF		9	HPV	E6	45	A
NYACTELKL		9	HPV	E6	47	A
NFACTELKF		9	HPV	E6	47	A
PYAVCRVCF		9	HPV	E6	62	A
LYYSKVRKY		9	HPV	E6	71	A
LFYSKVRKF		9	HPV	E6	71	A
VYDFVFADF		9	HPV	E6	42	A
VYADLRIVY		9	HPV	E6	46	A
VFADLRIVF		9	HPV	E6	46	A
NYSLYGDTF		9	HPV	E6	80	A
RFHNISGRF		9	HPV	E6	124	A
LYNLLIRCF		9	HPV	E6	98	A
FYSKVSEF		8	HPV	E6	69	
VYREGNPF		8	HPV	E6	53	
VFEFAFKDLF		10	HPV	E6	44	
EYRHYCYSLY		10	HPV	E6	82	
EYRHYNYSLY		10	HPV	E6	75	
ETRHYCYSLY		10	HPV	E6	82	A
EYDHYCYSLY		10	HPV	E6	82	A
KTRYYDYSVY		10	HPV	E6	78	A
KYDYYDYSVY		10	HPV	E6	78	A
ETRHYNYSLY		10	HPV	E6	75	A
EYDHYNYSLY		10	HPV	E6	75	A
TYCCKCDSTL		10	HPV	E7	56	A
TFCCKCDSTF		10	HPV	E7	56	A
TYCHSCDSTF		10	HPV	E7	58	A
CYTCGTTVRF		10	HPV	E7	59	A
LYPEPTDLF		9	HPV	E7	15	A
NYYIVTCCF		9	HPV	E7	52	A
LFLNTLSF		8	HPV	E7	89	
LFLSTLSF		8	HPV	E7	90	
RVLPPNWKY		9	Human	40s ribo prot S13	132	
RLAHEVGWKY		10	Human	60s ribo prot L13A	139	
AYKKQFSQY		9	Human	60s ribo prot L5	217	
KTKDIVNGL		9	Human	Factin capping protein	235	
SLFVSNHAY		9	Human	fructose biphosphatealdolase	355	
TYGPGPGSLSF		11	Human	Her2/neu	63	A
TYLGPGPGLSF		11	Human	Her2/neu	63	A
TYLPGPGPGSF		11	Human	Her2/neu	63	A
TYLPTGPGPGF		11	Human	Her2/neu	63	A
RWGLLLALL		9	Human	Her2/neu	8	

HLA-A24 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
PYVSRLLGI		9	Human	Her2/neu	780	
TYLPTNASL		9	Human	Her2/neu	63	
IYGPGPGLIF		10	Human	MAGE3	195	A
IYPGPGPGIF		10	Human	MAGE3	195	A
IYPKGPGPGF		10	Human	MAGE3	195	A
RISGVDRYY		9	Human	NADH ubiqoxidoreductase	53	
LYSACFWWL		9	Human	OA1	194	
LYSACFWWF		9	Human	OA1	194	A
TYSVSFDSLF		10	Human	PSM	624	
TYGPGPGSLF		10	Human	PSM	624	A
TYSGPGPGLF		10	Human	PSM	624	A
TYSVGPGPGF		10	Human	PSM	624	A
AYPNVSAKI		9	Lysteria	listeriolysin	196	
AYGPGPGKI		9	Lysteria	listeriolysin	196	A
IMVLSFLF		8	Pf	CSP	427	
YYGKQENW		8	Pf	CSP	55	
VFNVVNSSI		9	Pf	CSP	416	
ALFQEYQCY		9	Pf	CSP	18	
LYNTEKGRHPF		11	Pf	EXP	100	
YFILVNLL		8	Pf	LSA	10	
KFFDKDKEL		9	Pf	LSA	76	
KFIKSLFHI		9	Pf	LSA	1876	
YFILVNLLIF		10	Pf	LSA	10	
FYFILVNLLIF		11	Pf	LSA	9	
SFYFILVNLLI		11	Pf	LSA	8	
VFLIFFDLF		9	Pf	SSP2	13	
LYLLMDCSGSI		11	Pf	SSP2	49	
KVSDEIWNY		9	Pf		182	
SYKSSKRDKF		10	Pf		225	
RYQDPQNYEL		10	Pf		21	
DFFLKSKFNI		10	Pf		3	
IFHFFLFLL		9	Pf		11	
VFLVFSNVL		9	Pf		41	
TYGIIVPVL		9	Pf		160	
NYMKIMNHL		9	Pf		34	
TYKKKNNHI		9	Pf		264	
VYYNILIVL		9	Pf		277	
LYYLFNQHI		9	Pf		285	
SFFMNRFYI		9	Pf		310	
FYITTRYKY		9	Pf		316	
KYINFINFI		9	Pf		328	
KYEALIKLL		9	Pf		380	
IYYFDGNSW		9	Pf		40	
VYRHCEYIL		9	Pf		94	
TWKPTIFLL		9	Pf		135	
SYKVNCINF		9	Pf		168	

HLA-A24 SUPERTYPE						
Sequence	**SEQ ID NO.**	**AA**	**Organism**	**Protein**	**Position**	**Analog**
KYNYFIHFF		9	Pf		216	
NYFIHFFTW		9	Pf		218	
HFFTWGTMF		9	Pf		222	
MFVPKYFEL		9	Pf		229	
IYTIIQDQL		9	Pf		295	
FFLKSKFNI		9	Pf		4	
RMTSLKNEL		9	Pf		61	
YYNNFNNNY		9	Pf		77	
YYNKSTEKL		9	Pf		87	
EYEPTANLL		9	Pf		109	
VYXKHPVSX		9	Unknown	Naturally processed		A
TYGNXTVTV		9	Unknown	Naturally processed		A
KYPDRVVPX		9	Unknown	Naturally processed		A
VYVXSXVTX		9	Unknown	Naturally processed		A
DAQXXXNTX		9	Unknown	Naturally processed		A
KYQAVTTTL		9	Unknown	Tumor p198	197	
KYGPGPGTTTL		11	Unknown	Tumor p198	197	A
KYQGPGPGTTL		11	Unknown	Tumor p198	197	A

TABLE 18

HLA-A24 SUPERTYPE				
Sequence	**A*2402**	**A*2301**	**A*2902**	**A*3002**
AYGPGPGKF	2.4	9.7	44854	3.2
AYIGPGPGF	217	12	15887	5728
AYAAAAAAL	443			
AYSSWMYSY		21		4.9
DLLDTASALY			74	37
WFHISCLTF	204	11	95	75094
KYTSFPWL	208	177	>172413.7 9	346
FAAPFTQCGY			461	1364
SYQHFRKLLL	418	39	28	3768
LYSHPIILGF	2.6	5.4	109	1116
MSTTDLEAY			2565	396
MYVGDLCGSVF	26	0.91	612	1460
MYGPGPGGSVF	35	5.4	48442	31980
MYVGPGPGSVF	35	4.4	1527	28177
MYVGGPGPGVF	381	85	89	2870
MYVGDGPGPGF	90	11	8656	39608
VMGSSYGF	36	159	145	41967
EVDGVRLHRY			14940	113
KYSKSSIVGW	4061	491	>69444.44	>34482.76
KWSKSSIVGF	1674	84	>56179.78	30367
FFLKEKGGF	3456	655	3015	141
IYSKKRQEF	306	421	29353	727
IYSKKRQEIF	238	360	>131578.9 5	21001
LYVYHTQGYF	38	23	1696	1222
VYHTQGYFPDF	149	68	14923	>22556.39
RYPLTFGW	127	3836	13889	6251
RYPLTFGF	3.3	6.4	9704	6328
RFPLTFGF	178	124	12759	13472
TYGWCFKL	2181	333	25658	>8042.9
TFGWCFKF	3424	462	4449	>10135.14
LYVYHTQGY	7140	6088	216	258
NYTPGPGIRF	483	37	8334	>9646.3
QYPPLERLTL	211	22	>11520.74	>9646.3
QLPPLERLTF	2507	338	>37313.43	>36585.37
KYGSLQYLAL	2800	147	>69444.44	6957
LSKISEYRHY	>93023.26	>23671.5	55190	186
ISEYRHYNY	125794	>23557.69	1329	32
RFHNIRGRW	53237	11416	18	58
RFLSKISEY	472	121	34623	23
RFHNISGRW	>80536.91	22871	174	37
VYDFAFRDLCI	44	8.9	62242	35724
PYAVCDKCLKF	99	8.1	118249	>60000

HLA-A24 SUPERTYPE

Sequence	A*2402	A*2301	A*2902	A*3002
QYNKPLCDLLI	303	36	>166666.67	6680
PFGICKLCLRF	137	19	1249	32803
VYQFAFKDLCI	30	1.9	49276	3477
AYAACHKCIDF	91	14	1264	4699
VYKFLFTDLRI	37	14	30216	1865
PYGVCIMCLRF	380	100	69	43722
PYAVCRVCLLF	226	150	2711	53351
VYDFVFADLRI	47	8.0	8904	7585
QYNKPLCDLF	115	21	7658	525
VYEFAFKDLF	15	1.7	1973	2038
FYSKVSEFRF	7.1	2.2	79	18453
VYREGNPFGF	197	91	11120	21947
FYSRIRELRF	11	1.6	83	12598
PYAVCRVCLF	12	4.5	407	5226
FYSKVRKYRF	18	13	3042	1232
LYGDTLEQTF	91	24	40871	42025
VYDFAFRDF	9.6	19	47381	8490
AYRDLCIVY	2094	1479	7117	66
AFRDLCIVF	1005	369	6722	3305
PYAVCDKCF	216	183	122025	9884
KYYSKISEY	10951	2165	702	1.3
KFYSKISEF	174	138	73339	306
CYSLYGTTF	28	11	2088	7823
RYHNIRGRW	145	14	122644	15
RFHNIRGRF	29	2.4	346	0.69
VYCKTVLEF	50	4.7	610	1139
AYKDLFVVY	1549	905	639	1.3
AFKDLFVVF	294	6.8	3051	829
LYVVYRDSI	982	242	148359	3483
LFVVYRDSF	268	134	919	18
RYHNIAGHY	1227	195	138	0.93
RFHNIAGHF	37	17	635	1.4
VYGTTLEKF	19	13	75267	220
AYADLTVVY	369	1384	136	9.3
AFADLTVVF	203	30	779	137
RYLSKISEY	142	98	4247	1.1
NYSVYGNTF	28	29	9121	2559
RYHNISGRW	47	15	104884	13
AYKDLCIVY	33798	3036	5205	29
AFKDLCIVF	284	16	5846	2305
AYAACHKCF	200	159	10972	3393
VYGETLEKF	45	14	91902	20009
RYHSIAGQY	3170	1904	544	1.4
RFHSIAGQF	28	2.9	481	1.2
KYLFTDLRI	108	1.9	78575	339
KFLFTDLRF	12	0.74	44	152

HLA-A24 SUPERTYPE

Sequence	A*2402	A*2301	A*2902	A*3002
LYTDLRIVY	1986	1216	4.8	2.1
LFTDLRIVF	169	2.6	164	2649
PYGVCIMCF	190	147	144402	38850
RFLSKISEF	58	2.5	40103	201
EYRHYQYSF	21	2.3	13707	430
RYHNIMGRW	29	12	106990	7.1
RFHNIMGRF	39	2.6	174	1.3
VYNFACTEF	14	2.1	774	784
NYACTELKL	1741	131	77844	49107
NFACTELKF	211	13	46	6826
PYAVCRVCF	429	257	5602	316
LYYSKVRKY	21942	2735	1452	28
LFYSKVRKF	2008	277	11172	632
VYDFVFADF	9.9	2.2	1230	3961
VYADLRIVY	28	122	8.2	8.3
VFADLRIVF	23	2.5	87	24062
NYSLYGDTF	6.4	142	20945	64
RFHNISGRF	34	5.5	572	2.8
LYNLLIRCF	47	15	17958	2255
FYSKVSEF	21	18	3774	66667
VYREGNPF	554	147	10001	65970
VFEFAFKDLF	400			
EYRHYCYSLY			198	3.7
EYRHYNYSLY			956	12
ETRHYCYSLY			755	10
EYDHYCYSLY			799	77
KTRYYDYSVY			87841	0.71
KYDYYDYSVY			5749	11
ETRHYNYSLY			5464	29
EYDHYNYSLY			777	93
TYCCKCDSTL	206	30	145803	16588
TFCCKCDSTF	25	14	501	1167
TYCHSCDSTF	14	2.9	5236	3580
CYTCGTTVRF	41	18	7744	38331
LYPEPTDLF	38	17	1150	30732
NYYIVTCCF	27	12	2675	8398
LFLNTLSF	587	104	1013	118217
LFLSTLSF	2283	160	1034	>75000
RVLPPNWKY		>49000		3.0
RLAHEVGWKY		4631		3.8
AYKKQFSQY		10669		5.3
KTKDIVNGL		>49000		164
SLFVSNHAY		30295		1.1
TYGPGPGSLSF	7.1	1.7	9853	47246
TYLGPGPGLSF	23	0.65	600	26889
TYLPGPGPGSF	8.8	2.2	56183	7275
TYLPTGPGPGF	39	8.6	56574	32985

HLA-A24 SUPERTYPE

Sequence	A*2402	A*2301	A*2902	A*3002
RWGLLLALL	106	100	61253	300
PYVSRLLGI	11	18	200160	65465
TYLPTNASL	141	7.8	106153	8244
IYGPGPGLIF	7.4	8.0	58	6845
IYPGPGPGIF	58	12	18659	17959
IYPKGPGPGF	7.5	4.9	53603	61283
RISGVDRYY		>49000		3.0
LYSACFWWL	28			
LYSACFWWF	28			
TYSVSFDSLF	10	12	521	5218
TYGPGPGSLF	3.9	8.7	7228	10871
TYSGPGPGLF	50	92	7726	3461
TYSVGPGPGF	332	340	120913	55200
AYPNVSAKI	14	45	56905	4456
AYGPGPGKI	36	169	>156250	5427
IMVLSFLF	469	7.5	111	30000
YYGKQENW	85	951	>50000	>30000
VFNVVNSSI	403	35	24001	15737
ALFQEYQCY			149	1032
LYNTEKGRHPF	175	1947	>50000	>30000
YFILVNLL	96	82	4050	30000
KFFDKDKEL	269	>49000	>50000	3012
KFIKSLFHI	4.1	2.0	>50000	3495
YFILVNLLIF	577	12	764	3388
FYFILVNLLIF	599	50	902	9826
SFYFILVNLLI	229	35	3066	2096
VFLIFFDLF	40	12	1510	13554
LYLLMDCSGSI	154	10	5893	1469
KVSDEIWNY	52169	>11980.44	230	1.9
SYKSSKRDKF	256	797	12594	88
RYQDPQNYEL	212	124	79717	189
DFFLKSKFNI	1648	304	47714	491
IFHFFLFLL	208	80	1405	837
VFLVFSNVL	26	4.9	33675	37689
TYGIIVPVL	248	20	30056	1519
NYMKIMNHL	16	1.7	45443	110
TYKKKNNHI	30	81	21642	162
VYYNILIVL	265	52	>192307.6 9	1127
LYYLFNQHI	33	1.4	20130	11035
SFFMNRFYI	172	11	200	1022
FYITTRYKY	350	11	9.6	7.5
KYINFINFI	11	0.72	25475	55
KYEALIKLL	2856	484	17296	16098
IYYFDGNSW	80	6.1	3101	3025
VYRHCEYIL	2200	64	117851	3326
TWKPTIFLL	148	11	21155	306

HLA-A24 SUPERTYPE				
Sequence	**A*2402**	**A*2301**	**A*2902**	**A*3002**
SYKVNCINF	27	15	2535	572
KYNYFIHFF	2.5	0.49	319	2.7
NYFIHFFTW	9.3	1.3	9774	3020
HFFTWGTMF	83	5.7	4.0	220
MFVPKYFEL	266	11	2560	8560
IYTIIQDQL	72	45	>37313.43	14124
FFLKSKFNI	1434	49	43105	>83333.33
RMTSLKNEL	12711	1807	40270	14
YYNNFNNNY	817	126	19	34
YYNKSTEKL	109	106	55636	21751
EYEPTANLL	127	44	>37313.43	>26086.96
VYXKHPVSX	4.3			
TYGNXTVTV	26			
KYPDRVVPX	224			
VYVXSXVTX	5.3			
DAQXXXNTX	5.9			
KYQAVTTTL	22	16	>156250	625
KYGPGPGTTTL	103	130	9180	7056
KYQGPGPGTTL	543	438	74453	5999

TABLE 19

HLA-B7 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
APGPGPGLL		9	Artificial sequence	Consensus		A
APRGPGPGL		9	Artificial sequence	Consensus		A
QPRAPIRPI		9	EBNA		881	
YPLHEQHGM		9	EBNA		458	
CPTVQASKL		9	HBV	NUC	14	
SPTYKAFL		8	HBV	pol	659	
SPGPGPGL		8	HBV	pol	659	A
TPAGPGPGVF		10	HBV	pol	354	A
TPARGPGPGF		10	HBV	pol	354	A
TPTGWGLAI		9	HBV	POL	691	
APCNFFTSA		9	HBV	X	146	
GPGHKARVI		9	HIV	GAG	390	A
RPQVPLRPMTI		11	HIV	NEF	98	A
FPVRPQVPI		9	HIV	NEF	94	A
RPQVPLRPI		9	HIV	NEF	98	A
RPQVPLRPMTI		11	HIV	NEF	98	A
YPLTFGWCI		9	HIV	NEF	217	A
FPLTFGWCI		9	HIV	NEF	217	A
FPLTFGWCFKI		11	HIV	NEF	217	A
FPVRPQVPL		9	HIV	nef	94	
FPGPGPGPL		9	HIV	nef	94	A
FPVGPGPGL		9	HIV	nef	94	A
GPKVKQWPI		9	HIV	POL	197	A
LPPLERLTI		9	HIV	REV	79	A
CPEEKQRHL		9	HPV	E6	118	
VPGPGPGL		8	Human	Her2/neu	884	A
RPGPGPGVSEF		11	Human	Her2/neu	966	A
RPRGPGPGSEF		11	Human	Her2/neu	966	A
RPRFGPGPGEF		11	Human	Her2/neu	966	A
RPRFRGPGPGF		11	Human	Her2/neu	966	A
APGPGPGAAPA		11	Human	p53	76	A
APAGPGPGAPA		11	Human	p53	76	A
APAAGPGPGPA		11	Human	p53	76	A
APAAPGPGPGA		11	Human	p53	76	A
RPRGDNFAV		9	Pf	SSP2	305	
RPGPGPGAV		9	Pf	SSP2	305	A
RPRGPGPGV		9	Pf	SSP2	305	A
APRTVALTAL		10	Unknown	Naturally procesed		
APGPGPGTAL		10	Unknown	Naturally procesed		A
APRGPGPGAL		10	Unknown	Naturally procesed		A
APRTGPGPGL		10	Unknown	Naturally procesed		A
XVXDNATEY		9	Unknown	Naturally procesed		A
LGFVFTLTV		9	unknown			

TABLE 20

HLA-B7 SUPERTYPE

Sequence	SEQ ID NO.	B*0702	B*3501	B*5101	B*5301	B*5401
APGPGPGLL		299	7481	1614	18117	15613
APRGPGPGL		4.9	974	633	19779	1120
QPRAPIRPI		6770	>72000	>55000	12	>100000
YPLHEQHGM		>55000	20785	>55000	10	>100000
CPTVQASKL		3247	645	448	1861	21643
SPTYKAFL		109	31169	4665	54879	58651
SPGPGPGL		173	2337	3535	25607	53272
TPAGPGPGVF		334	374	296	2629	351
TPARGPGPGF		144	1678	2418	2742	31768
TPTGWGLAI		76	5145	103	1343	172
APCNFFTSA		43	8087	1045	>22409.64	0.61
GPGHKARVI		1686	>72000	>55000	2.2	>50000
RPQVPLRPMTI		47009	>18997.36	8081	21518	129
FPVRPQVPI		94	124	39	222	9.1
RPQVPLRPI		367	>23225.81	>9001.64	85335	1215
RPQVPLRPMTI		140	10455	5045	21538	>15128.59
YPLTFGWCI		54283	1378	153	154	79
FPLTFGWCI		47951	164	63	36	14
FPLTFGWCFKI		52567	4991	590	188	105
FPVRPQVPL		17	3.8	18	49	21
FPGPGPGPL		1584	426	2330	21036	29900
FPVGPGPGL		106	14	138	32	246
GPKVKQWPI		5500	>72000	>55000	2.3	>50000
LPPLERLTI		24398	13399	359	2624	11243
CPEEKQRHL		10	>52554.74	>35483.87	>109411.76	>76923.08
VPGPGPGL		1517	447	537	4094	46405
RPGPGPGVSEF		119	18115	16774	20988	3360
RPRGPGPGSEF		11	24871	>14824.8	19336	2745
RPRFGPGPGEF		14	>30901.29	>14824.8	76844	15470
RPRFRGPGPGF		9.7	>30901.29	>14824.8	49682	60095
APGPGPGAAPA		1112	1252	1317	4366	361
APAGPGPGAPA		161	>28915.66	11947	>39743.59	43
APAAGPGPGPA		173	12845	12470	28574	204
APAAPGPGPGA		811	3484	15814	>39240.51	158
RPRGDNFAV		12	20386	1681	>46268.66	212
RPGPGPGAV		23	48487	2899	>46268.66	1891
RPRGPGPGV		11	2368	52	34831	47
APRTVALTAL		12	4351	14601	61596	16804
APGPGPGTAL		81	16315	16462	>43661.97	35965
APRGPGPGAL		11	23381	12732	>43661.97	1665
APRTGPGPGL		15	1414	1559	22012	2043
XVXDNATEY		>55000	444			>100000
LGFVFTLTV		849	>72000	27500	>93000	464

TABLE 21

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
SEAAYAKKI		9	Artificial sequence	pool consensus		A
GEFPYKAAA		9	Artificial sequence	pool consensus		A
SEAPYKAIL		9	Artificial sequence	pool consensus		A
SEAPKYAIL		9	Artificial sequence	pool consensus		A
AEFKYIAAV		9	Artificial sequence	pool consensus		A
AEIPYLAKY		9	Artificial sequence	pool consensus		A
AEIPKLAYF		9	Artificial sequence	pool consensus		A
FPFDYAAAF		9	Artificial sequence			A
FPFKYKAAF		9	Artificial sequence			A
FPFKYAKAF		9	Artificial sequence			A
FPFKYAAAF		9	Artificial sequence			A
FAFKYAAAF		9	Artificial sequence			A
FQFKYAAAF		9	Artificial sequence			A
FDFKYAAAF		9	Artificial sequence			A
SENDRYRLL		9	EBV	BZLF1	209	A
IEDPPYNSL		9	EBV	lmp2	200	A
YEANGNLI		8	Flu	HA	259	A
YEDLRVLSF		9	Flu	NP	338	A
SDYEGRLI		8	Flu	NP	50	
GEISPYPSL		9	Flu	NS1	158	A
MDIDPYKEF		9	HBV	NUC	30	
LDKGIKPY		8	HBV	POL	125	
ADLMGYIPL		9	HCV	core	131	
LDPYARVAI		9	HCV	NS5b	2663	A
AENLWVTVY		9	HIV	gp120	1	
KENLWVTVY		9	HIV	gp120	1	A
AEKLWVTVY		9	HIV	gp120	1	A
AENKWVTVY		9	HIV	gp120	1	A
AENLKVTVY		9	HIV	gp120	1	A
AENLWKTVY		9	HIV	gp120	1	A
AENLWVKVY		9	HIV	gp120	1	A
AENLWVTKY		9	HIV	gp120	1	A
AENLWVTVK		9	HIV	gp120	1	A
FENLWVTVY		9	HIV	gp120	1	A
VENLWVTVY		9	HIV	gp120	1	A
PENLWVTVY		9	HIV	gp120	1	A
NENLWVTVY		9	HIV	gp120	1	A
DENLWVTVY		9	HIV	gp120	1	A

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
TENLWVTVY		9	HIV	gp120	1	A
YENLWVTVY		9	HIV	gp120	1	A
ATNLWVTVY		9	HIV	gp120	1	A
AEFLWVTVY		9	HIV	gp120	1	A
AEVLWVTVY		9	HIV	gp120	1	A
AEPLWVTVY		9	HIV	gp120	1	A
AEDLWVTVY		9	HIV	gp120	1	A
AENLWVTVY		9	HIV	gp120	1	
AETLWVTVY		9	HIV	gp120	1	A
AENFWVTVY		9	HIV	gp120	1	A
AENVWVTVY		9	HIV	gp120	1	A
AENPWVTVY		9	HIV	gp120	1	A
AENDWVTVY		9	HIV	gp120	1	A
AENNWVTVY		9	HIV	gp120	1	A
AENTWVTVY		9	HIV	gp120	1	A
AENLFVTVY		9	HIV	gp120	1	A
AENLVVTVY		9	HIV	gp120	1	A
AENLPVTVY		9	HIV	gp120	1	A
AENLDVTVY		9	HIV	gp120	1	A
AENLNVTVY		9	HIV	gp120	1	A
AENLTVTVY		9	HIV	gp120	1	A
AENLWFTVY		9	HIV	gp120	1	A
AENLWLTVY		9	HIV	gp120	1	A
AENLWPTVY		9	HIV	gp120	1	A
AENLWDTVY		9	HIV	gp120	1	A
AENLWNTVY		9	HIV	gp120	1	A
AENLWTTVY		9	HIV	gp120	1	A
AENLWVFVY		9	HIV	gp120	1	A
AENLWVVVY		9	HIV	gp120	1	A
AENLWVPVY		9	HIV	gp120	1	A
AENLWVDVY		9	HIV	gp120	1	A
AENLWVNVY		9	HIV	gp120	1	A
AENLWVSVY		9	HIV	gp120	1	A
AENLWVTFY		9	HIV	gp120	1	A
AENLWVTLY		9	HIV	gp120	1	A
AENLWVTPY		9	HIV	gp120	1	A
AENLWVTDY		9	HIV	gp120	1	A
AENLWVTNY		9	HIV	gp120	1	A
AENLWVTTY		9	HIV	gp120	1	A
AENLWVTVA		9	HIV	gp120	1	A
AENLWVTVC		9	HIV	gp120	1	A
AENLWVTVE		9	HIV	gp120	1	A
AENLWVTVF		9	HIV	gp120	1	A
AENLWVTVG		9	HIV	gp120	1	A
AENLWVTVH		9	HIV	gp120	1	A
AENLWVTVI		9	HIV	gp120	1	A
AENLWVTVL		9	HIV	gp120	1	A
AENLWVTVM		9	HIV	gp120	1	A
AENLWVTVN		9	HIV	gp120	1	A
AENLWVTVP		9	HIV	gp120	1	A
AENLWVTVQ		9	HIV	gp120	1	A

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
AENLWVTVR		9	HIV	gp120	1	A
AENLWVTVS		9	HIV	gp120	1	A
AENLWVTVT		9	HIV	gp120	1	A
AENLWVTVV		9	HIV	gp120	1	A
AENLWVTVW		9	HIV	gp120	1	A
AENLWVTVY		9	HIV	gp120	1	
AENLYVTVF		9	HIV	gp120	1	A
TEPAAVGVGAV		11	HIV	NEF	33	
AEPAAEGV		8	HIV	NEF	34	
AEPAAEGVGA		10	HIV	NEF	34	
AEPAAEGVGAV		11	HIV	NEF	34	
QEEEEVGFPV		10	HIV	NEF	84	
EEEEVGFPV		9	HIV	NEF	86	
EEEVGFPV		8	HIV	NEF	87	
EEVGFPVRPQV		11	HIV	NEF	88	
DEEVGFPV		8	HIV	NEF	89	
KEKGGLDGL		9	HIV	NEF	120	
KEKGGLDGLI		10	HIV	NEF	120	
QEILDLWV		8	HIV	NEF	184	
QEILDLWVY		9	HIV	NEF	184	
AETFYVDGA		9	HIV	POL	629	
EEKPRTLHDL		10	HPV	E6	6	
NEILIRCII		9	HPV	E6	97	
QEKKRHVDL		9	HPV	E6	113	
AEGKEVLL		8	Human	CEA	46	
QELFIPNI		8	Human	CEA	282	
QELFISNI		8	Human	CEA	460	
TEKNSGLY		8	Human	CEA	468	
AELPKPSI		8	Human	CEA	498	
PEAQNTTY		8	Human	CEA	525	
IESTPFNVA		9	Human	CEA	38	
AEGKEVLLL		9	Human	CEA	46	
EEATGQFRV		9	Human	CEA	132	
VEDKDAVAF		9	Human	CEA	157	
CEPETQDAT		9	Human	CEA	167	
PETQDATYL		9	Human	CEA	169	
CETQNPVSA		9	Human	CEA	215	
QELFIPNIT		9	Human	CEA	282	
AEPPKPFIT		9	Human	CEA	320	
VEDEDAVAL		9	Human	CEA	335	
CEPEIQNTT		9	Human	CEA	345	
PEIQNTTYL		9	Human	CEA	347	
YECGIQNEL		9	Human	CEA	391	
QELFISNIT		9	Human	CEA	460	
TEKNSGLYT		9	Human	CEA	468	
AEGKEVLLLV		10	Human	CEA	46	
KEVLLLVHNL		10	Human	CEA	49	
GERVDGNRQI		10	Human	CEA	70	
REIIYPNASL		10	Human	CEA	98	
NEEATGQFRV		10	Human	CEA	131	
EEATGQFRVY		10	Human	CEA	132	

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
GENLNLSCHA		10	Human	CEA	252	
QELFIPNITV		10	Human	CEA	282	
CEPEIQNTTY		10	Human	CEA	345	
PEIQNTTYLW		10	Human	CEA	347	
CEPEAQNTTY		10	Human	CEA	523	
PEAQNTTYLW		10	Human	CEA	525	
MESPSAPPHRW		11	Human	CEA	1	
IESTPFNVAEG		11	Human	CEA	38	
GERVDGNRQII		11	Human	CEA	70	
REIIYPNASLL		11	Human	CEA	98	
NEEATGQFRVY		11	Human	CEA	131	
CEPETQDATYL		11	Human	CEA	167	
GENLNLSCHAA		11	Human	CEA	252	
CEPEIQNTTYL		11	Human	CEA	345	
PEIQNTTYLWW		11	Human	CEA	347	
YECGIQNELSV		11	Human	CEA	391	
NELSVDHSDPV		11	Human	CEA	397	
CEPEAQNTTYL		11	Human	CEA	523	
PEAQNTTYLWW		11	Human	CEA	525	
PEIQNTTYLWWV		12	Human	CEA	347	
PEAQNTTYLWW V		12	Human	CEA	525	
CEPEIQNTTYLW W		13	Human	CEA	345	
AEMGKGSFKY		10	Human	elong. Factor Tu	48	
SEDCQSL		7	Human	Her2/neu	209	
REVRAVT		7	Human	Her2/neu	351	
FETLEEI		7	Human	Her2/neu	400	
TELVEPL		7	Human	Her2/neu	694	
SECRPRF		7	Human	Her2/neu	963	
PETHLDML		8	Human	Her2/neu	39	
QEVQGYVL		8	Human	Her2/neu	78	
RELQLRSL		8	Human	Her2/neu	138	
CELHCPAL		8	Human	Her2/neu	264	
LEEITGYL		8	Human	Her2/neu	403	
EEITGYLY		8	Human	Her2/neu	404	
DECVGEGL		8	Human	Her2/neu	502	
AEQRASPL		8	Human	Her2/neu	644	
KEILDEAY		8	Human	Her2/neu	765	
EEAPRSPL		8	Human	Her2/neu	1068	
SEDPTVPL		8	Human	Her2/neu	1113	
MELAALCRW		9	Human	Her2/neu	1	
QEVQGYVLI		9	Human	Her2/neu	78	
FEDNYALAV		9	Human	Her2/neu	108	
RELQLRSLT		9	Human	Her2/neu	138	
TEILKGGVL		9	Human	Her2/neu	146	
HEQCAAGCT		9	Human	Her2/neu	237	
CELHCPALV		9	Human	Her2/neu	264	
FESMPNPEG		9	Human	Her2/neu	279	
QEVTAEDGT		9	Human	Her2/neu	320	
CEKCSKPCA		9	Human	Her2/neu	331	
MEHLREVRA		9	Human	Her2/neu	347	

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
REVRAVTSA		9	Human	Her2/neu	351	
QEFAGCKKI		9	Human	Her2/neu	362	
EEITGYLYI		9	Human	Her2/neu	404	
RELGSGLAL		9	Human	Her2/neu	459	
GEGLACHQL		9	Human	Her2/neu	506	
QECVEECRV		9	Human	Her2/neu	538	
VEECRVLQG		9	Human	Her2/neu	541	
EECRVLQGL		9	Human	Her2/neu	542	
AEQRASPLT		9	Human	Her2/neu	644	
QETELVEPL		9	Human	Her2/neu	692	
VEPLTPSGA		9	Human	Her2/neu	697	
TELRKVKVL		9	Human	Her2/neu	718	
GENVKIPVA		9	Human	Her2/neu	743	
KEILDEAYV		9	Human	Her2/neu	765	
DEAYVMAGV		9	Human	Her2/neu	769	
DETEYHADG		9	Human	Her2/neu	873	
LESILRRRF		9	Human	Her2/neu	891	
GERLPQPPI		9	Human	Her2/neu	938	
LEDDDMGDL		9	Human	Her2/neu	1009	
EEYLVPQQG		9	Human	Her2/neu	1021	
EEEAPRSPL		9	Human	Her2/neu	1067	
EEAPRSPLA		9	Human	Her2/neu	1068	
SEGAGSDVF		9	Human	Her2/neu	1078	
PEYVNQPDV		9	Human	Her2/neu	1137	
PEYLTPQGG		9	Human	Her2/neu	1194	
PERGAPPST		9	Human	Her2/neu	1228	
AENPEYLGL		9	Human	Her2/neu	1243	
MELAALCRWG		10	Human	Her2/neu	1	
LELTYLPTNA		10	Human	Her2/neu	60	
QEVQGYVLIA		10	Human	Her2/neu	78	
FEDNYALAVL		10	Human	Her2/neu	108	
TEILKGGVLI		10	Human	Her2/neu	146	
GESSEDCQSL		10	Human	Her2/neu	206	
SEDCQSLTRT		10	Human	Her2/neu	209	
CELHCPALVT		10	Human	Her2/neu	264	
MEHLREVRAV		10	Human	Her2/neu	347	
QEFAGCKKIF		10	Human	Her2/neu	362	
FETLEEITGY		10	Human	Her2/neu	400	
LEEITGYLYI		10	Human	Her2/neu	403	
RELGSGLALI		10	Human	Her2/neu	459	
PEDECVGEGL		10	Human	Her2/neu	500	
QECVEECRVL		10	Human	Her2/neu	538	
VEECRVLQGL		10	Human	Her2/neu	541	
REYVNARHCL		10	Human	Her2/neu	552	
PECQPQNGSV		10	Human	Her2/neu	565	
EEGACQPCPI		10	Human	Her2/neu	619	
QETELVEPLT		10	Human	Her2/neu	692	
VEPLTPSGAM		10	Human	Her2/neu	697	
KETELRKVKV		10	Human	Her2/neu	716	
TELRKVKVLG		10	Human	Her2/neu	718	
GENVKIPVAI		10	Human	Her2/neu	743	

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
KEILDEAYVM		10	Human	Her2/neu	765	
DEAYVMAGVG		10	Human	Her2/neu	769	
DETEYHADGG		10	Human	Her2/neu	873	
TEYHADGGKV		10	Human	Her2/neu	875	
LESILRRRFT		10	Human	Her2/neu	891	
REIPDLLEKG		10	Human	Her2/neu	929	
SECRPRFREL		10	Human	Her2/neu	963	
RELVSEFSRM		10	Human	Her2/neu	970	
NEDLGPASPL		10	Human	Her2/neu	991	
AEEYLVPQQG		10	Human	Her2/neu	1020	
EEYLVPQQGF		10	Human	Her2/neu	1021	
SEEEAPRSPL		10	Human	Her2/neu	1066	
EEEAPRSPLA		10	Human	Her2/neu	1067	
SETDGYVAPL		10	Human	Her2/neu	1122	
PERGAPPSTF		10	Human	Her2/neu	1228	
PEYLGLDVPV		10	Human	Her2/neu	1246	
MELAALCRWGL		11	Human	Her2/neu	1	
PETHLDMLRHL		11	Human	Her2/neu	39	
RELQLRSLTEI		11	Human	Her2/neu	138	
GESSEDCQSLT		11	Human	Her2/neu	206	
SEDCQSLTRTV		11	Human	Her2/neu	209	
CELHCPALVTY		11	Human	Her2/neu	264	
FESMPNPEGRY		11	Human	Her2/neu	279	
CEKCSKPCARV		11	Human	Her2/neu	331	
MEHLREVRAVT		11	Human	Her2/neu	347	
REVRAVTSANI		11	Human	Her2/neu	351	
QEFAGCKKIFG		11	Human	Her2/neu	362	
FETLEEITGYL		11	Human	Her2/neu	400	
EEITGYLYISA		11	Human	Her2/neu	404	
GEGLACHQLCA		11	Human	Her2/neu	506	
DEEGACQPCPI		11	Human	Her2/neu	618	
AEQRASPLTSI		11	Human	Her2/neu	644	
TELVEPLTPSG		11	Human	Her2/neu	694	
KETELRKVKVL		11	Human	Her2/neu	716	
KEILDEAYVMA		11	Human	Her2/neu	765	
LEDVRLVHRDL		11	Human	Her2/neu	836	
WELMTFGAKPY		11	Human	Her2/neu	913	
GERLPQPPICT		11	Human	Her2/neu	938	
SECRPRFRELV		11	Human	Her2/neu	963	
RELVSEFSRMA		11	Human	Her2/neu	970	
AEEYLVPQQGF		11	Human	Her2/neu	1020	
EEYLVPQQGFF		11	Human	Her2/neu	1021	
SEEEAPRSPLA		11	Human	Her2/neu	1066	
SEGAGSDVFDG		11	Human	Her2/neu	1078	
SETDGYVAPLT		11	Human	Her2/neu	1122	
REGPLPAARPA		11	Human	Her2/neu	1153	
VENPEYLTPQG		11	Human	Her2/neu	1191	
PEYLTPQGGAA		11	Human	Her2/neu	1194	
AENPEYLGLDV		11	Human	Her2/neu	1243	
LELTYLPTNASL		12	Human	Her2/neu	60	
RELQLRSLTEIL		12	Human	Her2/neu	138	

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
PEGRYTFGASCV		12	Human	Her2/neu	285	
LEEITGYLYISA		12	Human	Her2/neu	403	
EEITGYLYISAW		12	Human	Her2/neu	404	
PEADQCVACAH Y		12	Human	Her2/neu	579	
TELVEPLTPSGA		12	Human	Her2/neu	694	
TEYHADGGKVPI		12	Human	Her2/neu	875	
GERLPQPPICTI		12	Human	Her2/neu	938	
AEEYLVPQQGFF		12	Human	Her2/neu	1020	
PEGRYTFGASCV T		13	Human	Her2/neu	285	
CEKCSKPCARVC Y		13	Human	Her2/neu	331	
MEHLREVRAVTS A		13	Human	Her2/neu	347	
DECVGEGLACHQ L		13	Human	Her2/neu	502	
PECQPQNGSVTC F		13	Human	Her2/neu	565	
RENTSPKANKEIL		13	Human	Her2/neu	756	
REIPDLLEKGERL		13	Human	Her2/neu	929	
SEFSRMARDPQR F		13	Human	Her2/neu	974	
SEGAGSDVFDGD L		13	Human	Her2/neu	1078	
GEFGGYGSV		9	Human	Histactranf	127	A
LWQLNGRLEYTL KDR		15	Human	IFN-B	21	A
SEFQAAI		7	Human	MAGE2	103	
SEYLQLV		7	Human	MAGE2	155	
WEELSML		7	Human	MAGE2	222	
GEPHISY		7	Human	MAGE2	295	
LEARGEAL		8	Human	MAGE2	16	
QEEEGPRM		8	Human	MAGE2	90	
EEEGPRMF		8	Human	MAGE2	91	
VELVHFLL		8	Human	MAGE2	114	
AEMLESVL		8	Human	MAGE2	133	
SEYLQLVF		8	Human	MAGE2	155	
EEKIWEEL		8	Human	MAGE2	218	
LEARGEALG		9	Human	MAGE2	16	
GEALGLVGA		9	Human	MAGE2	20	
QEEEGPRMF		9	Human	MAGE2	90	
VELVHFLLL		9	Human	MAGE2	114	
REPVTKAEM		9	Human	MAGE2	127	
SEYLQLVFG		9	Human	MAGE2	155	
PEEKIWEEL		9	Human	MAGE2	217	
EELSMLEVF		9	Human	MAGE2	223	
FEGREDSVF		9	Human	MAGE2	231	
YEFLWGPRA		9	Human	MAGE2	269	
EEGLEARGEA		10	Human	MAGE2	13	
LEARGEALGL		10	Human	MAGE2	16	
VEVTLGEVPA		10	Human	MAGE2	46	
EEGPRMFPDL		10	Human	MAGE2	92	

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
REPVTKAEML		10	Human	MAGE2	127	
SEYLQLVFGI		10	Human	MAGE2	155	
VEVVPISHLY		10	Human	MAGE2	167	
EEKIWEELSM		10	Human	MAGE2	218	
WEELSMLEVF		10	Human	MAGE2	222	
FEGREDSVFA		10	Human	MAGE2	231	
QENYLEYRQV		10	Human	MAGE2	252	
YEFLWGPRAL		10	Human	MAGE2	269	
GEPHISYPPL		10	Human	MAGE2	295	
EEGLEARGEAL		11	Human	MAGE2	13	
LEARGEALGLV		11	Human	MAGE2	16	
GEALGLVGAQA		11	Human	MAGE2	20	
EEQQTASSSST		11	Human	MAGE2	34	
VEVTLGEVPAA		11	Human	MAGE2	46	
EEEGPRMFPDL		11	Human	MAGE2	91	
SEFQAAISRKM		11	Human	MAGE2	103	
VELVHFLLLKY		11	Human	MAGE2	114	
LESVLRNCQDF		11	Human	MAGE2	136	
VEVVPISHLYI		11	Human	MAGE2	167	
IEGDCAPEEKI		11	Human	MAGE2	211	
EEKIWEELSML		11	Human	MAGE2	218	
EELSMLEVFEG		11	Human	MAGE2	223	
LEVFEGREDSV		11	Human	MAGE2	228	
YEFLWGPRALI		11	Human	MAGE2	269	
EEQQTASSSSTL		12	Human	MAGE2	34	
QEEEGPRMFPDL		12	Human	MAGE2	90	
SEFQAAISRKMV		12	Human	MAGE2	103	
LESVLRNCQDFF		12	Human	MAGE2	136	
VEVVPISHLYIL		12	Human	MAGE2	167	
EEGLEARGEALGL		13	Human	MAGE2	13	
LEARGEALGLVGA		13	Human	MAGE2	16	
LESEFQAAISRKM		13	Human	MAGE2	101	
REPVTKAEMLESV		13	Human	MAGE2	127	
SEYLQLVFGIEVV		13	Human	MAGE2	155	
IEVVEVVPISHLY		13	Human	MAGE2	164	
VEVVPISHLYILV		13	Human	MAGE2	167	
MEVDPIGHLY		10	Human	MAGE3	167	
EEEGPSTF		8	Human	MAGE3	91	
AELVHFLL		8	Human	MAGE3	114	
FEGREDSI		8	Human	MAGE3	231	
QEAASSSST		9	Human	MAGE3	36	
AELVHFLLL		9	Human	MAGE3	114	
AEMLGSVVG		9	Human	MAGE3	133	
EELSVLEVF		9	Human	MAGE3	223	
FEGREDSIL		9	Human	MAGE3	231	
QEAASSSSTL		10	Human	MAGE3	36	
EEGPSTFPDL		10	Human	MAGE3	92	
IELMEVDPIG		10	Human	MAGE3	164	

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
MEVDPIGHLY		10	Human	MAGE3	167	
EEKIWEELSV		10	Human	MAGE3	218	
WEELSVLEVF		10	Human	MAGE3	222	
FEGREDSILG		10	Human	MAGE3	231	
EEEGPSTFPDL		11	Human	MAGE3	91	
AELVHFLLLKY		11	Human	MAGE3	114	
MEVDPIGHLYI		11	Human	MAGE3	167	
REGDCAPEEKI		11	Human	MAGE3	211	
EEKIWEELSVL		11	Human	MAGE3	218	
LEVFEGREDSI		11	Human	MAGE3	228	
RERFEMF		7	Human	p53	335	
LEDSSGNL		8	Human	p53	257	
GEYFTLQI		8	Human	p53	325	
VEPPLSQET		9	Human	p53	10	
PENNVLSPL		9	Human	p53	27	
DEAPRMPEA		9	Human	p53	61	
HERCSDSDG		9	Human	p53	179	
VEGNLRVEY		9	Human	p53	197	
VEYLDDRNT		9	Human	p53	203	
LEDSSGNLL		9	Human	p53	257	
RELNEALEL		9	Human	p53	342	
NEALELKDA		9	Human	p53	345	
LELKDAQAG		9	Human	p53	348	
MEEPQSDPSV		10	Human	p53	1	
VEPPLSQETF		10	Human	p53	10	
QETFSDLWKL		10	Human	p53	16	
IEQWFTEDPG		10	Human	p53	50	
DEAPRMPEAA		10	Human	p53	61	
HERCSDSDGL		10	Human	p53	179	
VEGNLRVEYL		10	Human	p53	197	
VEYLDDRNTF		10	Human	p53	203	
PEVGSDCTTI		10	Human	p53	223	
LEDSSGNLLG		10	Human	p53	257	
FEVRVCACPG		10	Human	p53	270	
TEEENLRKKG		10	Human	p53	284	
GEPHHELPPG		10	Human	p53	293	
GEYFTLQIRG		10	Human	p53	325	
RERFEMFREL		10	Human	p53	335	
FEMFRELNEA		10	Human	p53	338	
QETFSDLWKLL		11	Human	p53	16	
HERCSDSDGLA		11	Human	p53	179	
YEPPEVGSDCT		11	Human	p53	220	
HELPPGSTKRA		11	Human	p53	297	
FEMFRELNEAL		11	Human	p53	338	
NEALELKDAQA		11	Human	p53	345	
TEDPGPDEAPRM		12	Human	p53	55	
GEPHHELPPGST		12	Human	p53	293	
DEAPRMPEAAPP V		13	Human	p53	61	
YEPPEVGSDCTTI		13	Human	p53	220	
RERRDNYV		8	Human	unknown		

HLA-B44 SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
SEIDLILGY		9	Human	unknown		
AEIPTRVNY		9	Human	unknown		
AEMGKFKFSY		10	Human	unknown		
DEIGVIDLY		9	Human	unknown		
AEMGKFKYSF		10	Human	unknown		A
SEAIHTFQY		9	Human	unknown		
SEAIYTFQF		9	Human	unknown		A
AEGIVTGQY		9	Human	unknown		
HETTYNSI		8	Mouse	beta actin	275	A
GELSYLNV		8	Mouse	cathepsin D	255	
YEDTGKTI		8	Mouse	p40 phox RNA	245	
YENDIEKKI		9	Pf	CSP	375	

TABLE 22

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
SEAAYAKKI		8609	308	129	1685	61	287
GEFPYKAAA		286	170	3.9	746	2537	11
SEAPYKAIL		2258	29	8.8	440	170	262
SEAPKYAIL		2263	113	7.8	762	2260	479
AEFKYIAAV		48	2.8	6.5	28	21	4.9
AEIPYLAKY		116	7258	3159	44	30	668
AEIPKLAYF		1641	57	5.6	229	57	608
FPFDYAAAF		141					
FPFKYKAAF		155					
FPFKYAKAF		86					
FPFKYAAAF		16					
FAFKYAAAF		95					
FQFKYAAAF		22					
FDFKYAAAF		187					
SENDRYRLL		18281	271	23	183	164	1073
IEDPPYNSL		35457	16	688	15833	40075	18697
YEANGNLI		191	7.9	7.0	516	3085	10342
YEDLRVLSF		20	67	71	24	212	18697
SDYEGRLI		>24800	27150	86	851	228	10469
GEISPYPSL		19361	24	1.8	3564	293	115
MDIDPYKEF		169477	3700	382	21744	1949	2615
LDKGIKPY		>100000	17884	468	>43192.49	19311	23609
ADLMGYIPL		>7616.71	959	4.7	>21395.35	10292	>49000
LDPYARVAI		>24409.45	>88888.89	372	>41628.96	>39766.08	>49000
AENLWVTVY		155	1053	547	522	284	200
KENLWVTVY		184	2738	373	308	306	6215
AEKLWVTVY		286	18278	306	168	287	219
AENKWVTVY		781	11303	534	294	540	297
AENLKVTVY		138	7746	1075	253	487	9624
AENLWKTVY		913	850	406	139	383	245
AENLWVKVY		2735	1482	1696	708	105	132
AENLWVTKY		511	1010	1998	355	1064	201
AENLWVTVK		29464	853	2004	6305	2133	186
FENLWVTVY		59	943	1336	4179	1312	21403
VENLWVTVY		25	5499	5586	13454	4856	15654
PENLWVTVY		190	>72727.27	>154545.45	>167272.73	>425000	>49000
NENLWVTVY		38	>72727.27	11774	453	224	1668
DENLWVTVY		26	>72727.27	41098	4589	988	49000
TENLWVTVY		14	14040	1415	291	364	5296
YENLWVTVY		29	552	324	640	369	10701
ATNLWVTVY		17615	487	>154545.45	8912	>43037.97	>49000
AEFLWVTVY		131	183	240	1013	156	472
AEVLWVTVY		142	1549	436	1520	390	1244
AEPLWVTVY		310	1727	2484	1322	96	1384
AEDLWVTVY		354	423	3521	2329	469	1845
AENLWVTVY		122	1581	552	308	132	301
AETLWVTVY		199	1052	198	501	221	774
AENFWVTVY		182	1394	542	171	268	289
AENVWVTVY		262	2238	386	1112	744	737
AENPWVTVY		27	843	224	18	53	202

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
AENDWVTVY		324	954	742	96	165	365
AENNWVTVY		167	1161	357	214	162	99
AENTWVTVY		213	1451	1793	386	166	442
AENLFVTVY		29	970	334	357	125	232
AENLVVTVY		62	876	1344	1030	203	718
AENLPVTVY		20	205	566	356	126	246
AENLDVTVY		517	220	12081	673	340	1291
AENLNVTVY		198	564	3544	447	358	2445
AENLTVTVY		153	689	1269	327	208	793
AENLWFTVY		360	699	668	227	62	90
AENLWLTVY		666	1702	884	647	226	227
AENLWPTVY		661	690	688	157	50	116
AENLWDTVY		775	1145	2090	414	68	263
AENLWNTVY		336	1338	957	66	81	257
AENLWTTVY		196	246	625	51	50	118
AENLWVFVY		242	857	375	348	310	237
AENLWVVVY		326	2728	1688	599	632	468
AENLWVPVY		303	175	183	96	47	106
AENLWVDVY		415	700	3440	334	92	242
AENLWVNVY		317	1156	952	159	76	266
AENLWVSVY		232	1251	1347	351	178	292
AENLWVTFY		1299	1201	295	124	222	347
AENLWVTLY		392	463	731	199	119	349
AENLWVTPY		41	274	189	127	44	122
AENLWVTDY		1001	930	1208	191	103	328
AENLWVTNY		730	865	948	149	74	215
AENLWVTTY		28	280	191	37	26	48
AENLWVTVA		9689	557	4.8	1543	296	9.1
AENLWVTVC		178026	157	1425	5593	2267	146
AENLWVTVE		>258333.33	3888	1362	8910	2573	246
AENLWVTVF		365	162	20	346	162	262
AENLWVTVG		39743	861	47	1812	245	35
AENLWVTVH		16516	493	151	966	387	120
AENLWVTVI		11224	14	7.3	237	88	54
AENLWVTVL		6198	14	13	68	208	114
AENLWVTVM		508	13	6.1	195	35	50
AENLWVTVN		129167	6701	481	2623	414	169
AENLWVTVP		38441	9711	339	7715	2473	187
AENLWVTVQ		49640	522	85	1223	188	100
AENLWVTVR		32979	1246	1744	4857	1474	233
AENLWVTVS		25726	2163	103	4221	417	34
AENLWVTVT		12331	947	7.8	2696	343	10
AENLWVTVV		10709	84	19	5757	1432	35
AENLWVTVW		22610	1304	135	423	324	204
AENLWVTVY		51	1358	90	66	43	68
AENLYVTVF		61	17	3.1	39	47	69
TEPAAVGVGAV		>8115.18	930	391	1938	459	8235
AEPAAEGV		>8115.18	2070	2675	>22604.42	402	6590
AEPAAEGVGA		>8115.18	4116	1655	>22604.42	>11447.81	104
AEPAAEGVGAV		>8611.11	20364	242	>23896.1	>11447.81	1499
QEEEEVGFPV		>8611.11	13117	2596	15203	>11447.81	86
EEEEVGFPV		3691	3340	417	7440	10313	37

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
EEEVGFPV		427	9578	2605	6372	>10461.54	227
EEVGFPVRPQV		>22794.12	9905	108	23777	6553	808
DEEVGFPV		7.1	>32000	4260	9305	>10461.54	916
KEKGGLDGL		>22794.12	55	174	>81415.93	>10461.54	9926
KEKGGLDGLI		>22794.12	843	233	14726	3626	9986
QEILDLWV		>22794.12	142	1717	>81415.93	5919	5504
QEILDLWVY		52	740	4522	264	172	6261
AETFYVDGA		>6709.96	21630	1923	>21198.16	6924	38
EEKPRTLHDL		>81578.95	36208	34027	15236	30010	419
NEILIRCII		5672	291	59	2722	258	3248
QEKKRHVDL		7.3	15984	63093	443	211	12613
AEGKEVLL		11455	1311	5303	17268	129	14165
QELFIPNI		127	5815	147	752	8.5	1319
QELFISNI		889	6396	1175	2282	70	1172
TEKNSGLY		211	9851	7117	1868	605	10248
AELPKPSI		7423	6697	131	1164	19	2608
PEAQNTTY		149	2594	2437	2204	76	3255
IESTPFNVA		69	1234	66	18749	0.97	15
AEGKEVLLL		1080	72	147	178	1.7	199
EEATGQFRV		805	5563	470	1691	95	18
VEDKDAVAF		94	121	1583	1661	1443	21204
CEPETQDAT		4009	3646	410	23421	50	97
PETQDATYL		9473	1240	33745	>34586.47	301	13430
CETQNPVSA		73	7016	261	20023	10.0	15
QELFIPNIT		125	4361	172	1217	3.0	18
AEPPKPFIT		12850	7067	7170	>34586.47	232	1813
VEDEDAVAL		840	11	2665	30667	51	27810
CEPEIQNTT		6889	5709	3081	31834	120	2732
PEIQNTTYL		923	138	2786	16816	231	1825
YECGIQNEL		82	71	53	452	5.3	855
QELFISNIT		530	6571	58	2334	3.9	80
TEKNSGLYT		1113	7522	3195	10097	101	1963
AEGKEVLLLV		5135	1019	408	479	8.6	994
KEVLLLVHNL		893	3.1	4.4	414	2.3	2512
GERVDGNRQI		9395	1933	369	3900	13	19464
REIIYPNASL		741	2.3	7.5	374	1.7	954
NEEATGQFRV		998	29086	22678	4365	471	405
EEATGQFRVY		64	>33333.33	55956	29	1041	1374
GENLNLSCHA		14373	1341	357	8610	5.3	271
QELFIPNITV		81	121	27	93	2.6	14
CEPEIQNTTY		1459	>10322.58	35697	49	14596	43739
PEIQNTTYLW		819	3301	9423	13	6173	10011
CEPEAQNTTY		9525	>12903.23	>48571.43	61	>4268.68	17330
PEAQNTTYLW		17082	>9248.55	>12592.59	27	21243	>28654.97
MESPSAPPHRW		12	943	1915	5.3	41	359
IESTPFNVAEG		87	1074	352	89	8.7	84
GERVDGNRQII		764	278	18	871	1.3	27084
REIIYPNASLL		1788	2.4	12	57	0.38	1777
NEEATGQFRVY		7.7	3252	999	9.6	69	3986
CEPETQDATYL		831	311	3388	398	807	62150
GENLNLSCHAA		7838	4557	63	1907	9.0	32
CEPEIQNTTYL		129	287	1603	1245	60	11981

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
PEIQNTTYLWW		172	749	1045	17	227	1365
YECGIQNELSV		9.2	33	26	1714	0.46	155
NELSVDHSDPV		49	2554	1128	1615	38	78
CEPEAQNTTYL		962	2184	11723	3419	131	2450
PEAQNTTYLWW		147	2096	3090	121	79	2005
PEIQNTTYLWWV		644	1808	1539	481	93	994
PEAQNTTYLWWV		20	1694	646	5.1		3.3
CEPEIQNTTYLWW		84	858	3168	7.9	409	1243
AEMGKGSFKY		1618	6427	3820	112	90	305
SEDCQSL		18245	2691	14258	8248	431	19225
REVRAVT		8564	3136	725	31615	29	23544
FETLEEI		1518	7621	2110	42991	69	67957
TELVEPL		162	14164	1258	8854	66	>148484.85
SECRPRF		926	18181	1157	852	48	8856
PETHLDML		1954	8387	6118	>17523.81	83	20257
QEVQGYVL		3.4	28	5.0	1210	0.92	33
RELQLRSL		42	49	5.9	2025	0.62	1372
CELHCPAL		150	871	259	4361	39	30089
LEEITGYL		242	830	1805	5913	403	35502
EEITGYLY		20	5713	1223	11	83	238
DECVGEGL		49	4864	481	938	34	14244
AEQRASPL		16	73	13	211	0.38	120
KEILDEAY		82	921	430	1081	74	2646
EEAPRSPL		1191	3489	1611	1593	171	1926
SEDPTVPL		103	71	161	12267	2.0	308
MELAALCRW		7.0	4833	138	16	9.9	1183
QEVQGYVLI		77	206	39	30	0.50	96
FEDNYALAV		12	34	5.1	13470	0.17	131
RELQLRSLT		638	316	13	465	0.20	162
TEILKGGVL		125	30	14	1377	0.28	2480
HEQCAAGCT		1995	42164	7377	19048	178	2974
CELHCPALV		136	4805	319	2308	52	1110
FESMPNPEG		6068	30237	59	16458	14	155
QEVTAEDGT		5207	31081	3122	7886	66	1843
CEKCSKPCA		3740	27386	2703	19957	342	8007
MEHLREVRA		233	44754	386	38	3.2	19
REVRAVTSA		626	427	0.71	3160	0.18	9.3
QEFAGCKKI		1120	736	131	81	44	2684
EEITGYLYI		86	906	916	12	121	94
RELGSGLAL		359	3.7	0.85	457	0.97	2262
GEGLACHQL		13766	187	88	112	11	340
QECVEECRV		15799	8755	1664	7150	210	4542
VEECRVLQG		1528	8947	7622	14202	305	20142
EECRVLQGL		890	7076	2029	717	434	1185
AEQRASPLT		346	874	183	103	1.8	10
QETELVEPL		12	62	85	681	3.5	1232
VEPLTPSGA		7321	>9638.55	11	8516	191	17037
TELRKVKVL		1514	4698	54	2128	2.5	14147
GENVKIPVA		10755	14510	7.5	20309	2.7	7.0
KEILDEAYV		1358	62	146	6466	8.4	42
DEAYVMAGV		58	5327	1245	8006	138	161

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
DETEYHADG		159	>11940.3	>65384.62	>24403.18	1397	13353
LESILRRRF		29	>11940.3	3475	4.7	101	12918
GERLPQPPI		62	71	15	63	1.1	15
LEDDDMGDL		191	556	351	947	900	6251
EEYLVPQQG		66	10344	136	651	126	131
EEEAPRSPL		902	4490	2881	342	362	307
EEAPRSPLA		486	10707	4900	180	294	4.5
SEGAGSDVF		74	5627	6525	69	192	6960
PEYVNQPDV		831	3437	1581	1109	48	2536
PEYLTPQGG		1456	18951	13860	6532	284	18990
PERGAPPST		385	4744	7679	1116	178	7767
AENPEYLGL		17	81	271	44	2.5	155
MELAALCRWG		102	8684	1840	5.7	135	408
LELTYLPTNA		332	325	10.4	6428	3.1	24
QEVQGYVLIA		61	772	64	1871	15	11
FEDNYALAVL		321	6.2	48	2844	3.8	3095
TEILKGGVLI		1021	241	294	24	21	7600
GESSEDCQSL		138636	8.1	23	427	5.1	2491
SEDCQSLTRT		335	8550	11529	518	2857	4726
CELHCPALVT		80	>9248.55	65	933	18	477
MEHLREVRAV		72	20684	160	180	13	140
QEFAGCKKIF		53	3686	12	4.0	3.6	115
FETLEEITGY		671	53363	36302	262	1679	>28488.37
LEEITGYLYI		143	914	2996	222	143	1488
RELGSGLALI		4810	22	4.4	32	0.78	173
PEDECVGEGL		1257	278	257	6331	49	24019
QECVEECRVL		315	444	399	606	22	2863
VEECRVLQGL		270	227	5815	237	189	16094
REYVNARHCL		1327	39	4.8	106	0.97	126
PECQPQNGSV		7962	35957	20374	12964	472	>28488.37
EEGACQPCPI		119	40113	340	52	80	401
QETELVEPLT		15	293	338	1619	13	288
VEPLTPSGAM		4649	1667	584	4368	108	20167
KETELRKVKV		11925	26700	68	2936	4.5	1603
TELRKVKVLG		721	20312	601	3650	14	12816
GENVKIPVAI		563	314	28	230	6.7	198
KEILDEAYVM		0.14	10	153	35	7.5	234
DEAYVMAGVG		122	203	154	4033	4102	218
DETEYHADGG		613	45291	16801	3891	269	29025
TEYHADGGKV		239	5246	2003	2911	15	1571
LESILRRRFT		82	28476	1189	34	87	2251
REIPDLLEKG		649	4493	814	1270	13	1977
SECRPRFREL		80	307	18	11	0.20	25
RELVSEFSRM		9.1	28	4.3	33	0.12	1726
NEDLGPASPL		107	281	150	40	6.0	231
AEEYLVPQQG		723	66699	24424	417	479	127
EEYLVPQQGF		2.1	26569	2551	6.9	11	73
SEEEAPRSPL		151	155	217	37	8.4	84
EEEAPRSPLA		6611	49549	38943	425	960	14
SETDGYVAPL		94	214	184	386	2.4	302
PERGAPPSTF		1062	14884	3437	6871	208	15700
PEYLGLDVPV		613	352	35	1371	1.7	610

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
MELAALCRWGL		6.4	24	30	17	0.92	116
PETHLDMLRHL		1322	700	2971	11534	70	4329
RELQLRSLTEI		261	2.8	3.7	125	0.99	269
GESSEDCQSLT		742	48	180	14386	40	2158
SEDCQSLTRTV		101	4322	311	943	21	10
CELHCPALVTY		12	3469	3198	140	89	2779
FESMPNPEGRY		74	3666	3533	59	70	1394
CEKCSKPCARV		1167	4103	2079	9594	101	1561
MEHLREVRAVT		1064	3614	2207	795	111	74
REVRAVTSANI		4491	17	30	1680	1.8	421
QEFAGCKKIFG		211	314	477	37	2.1	138
FETLEEITGYL		133	78	649	7490	42	2200
EEITGYLYISA		0.94	1440	52	4.5	2.1	0.9
GEGLACHQLCA		62	39	97	159	2.7	196
DEEGACQPCPI		451	5517	7293	968	438	1323
AEQRASPLTSI		467	19	58	5.1	2.5	11
TELVEPLTPSG		601	2978	3703	>21052.63	269	14079
KETELRKVKVL		9529	2973	1868	7136	71	12237
KEILDEAYVMA		731	252	95	11514	64	123
LEDVRLVHRDL		729	325	641	818	59	2382
WELMTFGAKPY		13	509	778	24	75	1216
GERLPQPPICT		12486	24270	23	9094	3.9	15
SECRPRFRELV		1996	3673	121	927	18	118
RELVSEFSRMA		168	389	143	2613	3.5	32
AEEYLVPQQGF		125	584	1831	21	99	268
EEYLVPQQGFF		94	4291	1695	78	168	154
SEEEAPRSPLA		1318	3604	5110	8550	158	27
SEGAGSDVFDG		928	3751	5695	374	286	3008
SETDGYVAPLT		66	125	224	1225	2.2	45
REGPLPAARPA		157	543	78	32906	4.2	347
VENPEYLTPQG		8386	56393	42593	17337	11	4188
PEYLTPQGGAA		1724	41026	200	>17829.46	354	1382
AENPEYLGLDV		11934	28	139	69	3.0	24
LELTYLPTNASL		12	25	102	386	6.8	11
RELQLRSLTEIL		5954	151	600	3778	1.1	1371
PEGRYTFGASCV		4071	2.9	4.4	778		116
LEEITGYLYISA		209	28	31	263	18	694
EEITGYLYISAW		746	478	1800	252		1492
PEADQCVACAHY		901	4050	5127	213		463
TELVEPLTPSGA		236	2059	59	2132		206
TEYHADGGKVPI		680	22	4.4	2177		61
GERLPQPPICTI		17769	162	3.9	292		2.5
AEEYLVPQQGFF		144	228	45	16		13
PEGRYTFGASCVT		5228	3793	737	1419	267	673
CEKCSKPCARVCY		701	>53333.33	406	302	44	1315
MEHLREVRAVTSA		70	669	72	144	18	12
DECVGEGLACHQL		464	2635	3668	2544	212	2063
PECQPQNGSVTCF		6293	381	5338	3564	375	>22374.43
RENTSPKANKEIL		7750	3.7	77	>2540.03	3.9	1510
REIPDLLEKGERL		7636	40	136	3050	16	2710

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
SEFSRMARDPQRF		61	350	57	23	12	247
SEGAGSDVFDGDL		5172	45	2059	1303	711	2458
GEFGGYGSV		307	112	6.4	2335	534	40
LWQLNGRLEYTLKDR						0.11	
SEFQAAI		181	6830	779	2660	33	9597
SEYLQLV		1375	7777	658	733	21	930
WEELSML		1288	781	740	>28482.97	151	82009
GEPHISY		8833	12272	6716	36116	272	>33333.33
LEARGEAL		163	99	65	29495	2.9	31463
QEEEGPRM		298	11598	1608	19255	118	6730
EEEGPRMF		723	12281	32093	2406	213	943
VELVHFLL		5.0	69	31	3322	1.2	2427
AEMLESVL		968	14	31	327	0.88	302
SEYLQLVF		0.97	765	6.0	284	0.70	122
EEKIWEEL		753	9084	2599	98976	104	171
LEARGEALG		155	1161	3006	11018	24	2688
GEALGLVGA		9529	2832	34	6134	2.2	17
QEEEGPRMF		414	918	7747	237	409	2171
VELVHFLLL		71	79	31	579	3.1	1129
REPVTKAEM		60	373	284	896	4.5	832
SEYLQLVFG		18	8890	421	271	19	113
PEEKIWEEL		577	19449	3908	1029	235	17345
EELSMLEVF		1.4	16436	252	22	2.8	1013
FEGREDSVF		9.8	2366	348	221	13	3339
YEFLWGPRA		5.3	249	5.2	2355	1.1	241
EEGLEARGEA		1077	3434	3227	216	302	30
LEARGEALGL		81	184	277	2275	4.1	964
VEVTLGEVPA		14	371	31	3801	0.52	15
EEGPRMFPDL		128	4438	486	95	13	42
REPVTKAEML		88	23	264	84	41	917
SEYLQLVFGI		2.2	20	6.1	3.7	0.84	4.4
VEVVPISHLY		20	11522	4385	13	1225	4885
EEKIWEELSM		17	21450	477	46	19	107
WEELSMLEVF		0.14	463	30	15	15	290
FEGREDSVFA		178	>10062.89	4775	6879	192	503
QENYLEYRQV		118	493	102	17	16	27
YEFLWGPRAL			8.5	0.97	130	0.72	753
GEPHISYPPL		2612	7.0	2.9	1200	0.71	380
EEGLEARGEAL		179	300	578	2630	19	1812
LEARGEALGLV		158	198	345	>17829.46	13	1912
GEALGLVGAQA		877	4293	52	3575	1.4	28
EEQQTASSSST		752	4040	41162	5910	1552	134
VEVTLGEVPAA		124	25216	919	>23469.39	44	1583
EEEGPRMFPDL		1011	2646	3470	3273	131	209
SEFQAAISRKM		7.0	345	107	88	1.2	161
VELVHFLLLKY		52	550	294	1551	49	1790
LESVLRNCQDF		64	5409	3458	209	76	15241
VEVVPISHLYI		97	135	146	335	7.2	3788
IEGDCAPEEKI		844	27827	32058	2627	486	183
EEKIWEELSML		1641	4978	20625	1862	375	181

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
EELSMLEVFEG		1.5	24061	294	4.6	23	163
LEVFEGREDSV		639	2624	367	>21296.3	46	29449
YEFLWGPRALI		5.2	4.1	2.8	92	0.59	450
EEQQTASSSSTL		7259	166	526	57	981	15
QEEEGPRMFPDL		3595	394	1330	1643		120
SEFQAAISRKMV		43	161	29	25		21
LESVLRNCQDFF		56	55	356	184	24	1993
VEVVPISHLYIL		266	3.4	16	486	4.0	1182
EEGLEARGEALG L		10416	1769	5143	196	118	1673
LEARGEALGLVG A		347	20	48	2575	2.2	116
LESEFQAAISRKM		49	310	72	242	14	22
REPVTKAEMLES V		5531	337	411	4546	21	1507
SEYLQLVFGIEVV		9.7	23	4.5	144	5.4	6.6
IEVVEVVPISHLY		79	162	245	52	125	106
VEVVPISHLYILV		92	93	47	270	51	112
MEVDPIGHLY		13	209	334	13	28	228
EEEGPSTF		216	1008	435	3933	27	1819
AELVHFLL		120	71	6.8	1074	0.16	452
FEGREDSI		927	718	127	7708	13	2291
QEAASSSST		1422	23469	1480	9593	41	110
AELVHFLLL		160	25	3.1	33	0.94	141
AEMLGSVVG		96	1899	109	27	1.6	11
EELSVLEVF		7.3	10215	3314	61	12	2120
FEGREDSIL		1091	51	439	1925	11	>27071.82
QEAASSSSTL		171	49	47	56	13	287
EEGPSTFPDL		158	655	591	198	127	128
IELMEVDPIG		194	6592	5325	222	>16306.95	7604
MEVDPIGHLY		15	617	625	11	99	169
EEKIWEELSV		73	8947	79	396	17	17
WEELSVLEVF		1.7	75	37	14	13	1701
FEGREDSILG		229	940	4361	8534	172	20261
EEEGPSTFPDL		935	431	2120	2685	102	158
AELVHFLLLKY		153	32	39	178	1.6	670
MEVDPIGHLYI		9.8	34	16	64	0.91	95
REGDCAPEEKI		973	2418	830	4038	42	146
EEKIWEELSVL		133	152	1255	1416	58	218
LEVFEGREDSI		4745	206	512	20963	69	>31012.66
RERFEMF		180	4079	1907	25488	108	20048
LEDSSGNL		17736	782	362	42791	211	15946
GEYFTLQI		7774	112	60	3511	1.0	261
VEPPLSQET		8302	17052	20808	3186	236	29270
PENNVLSPL		1150	1261	718	11174	8.8	>27071.82
DEAPRMPEA		84	9092	4577	6448	98	10.0
HERCSDSDG		1118	2367	38636	19328	208	13390
VEGNLRVEY		832	12752	67730	142	2583	39059
VEYLDDRNT		1442	36833	35854	10071	157	13503
LEDSSGNLL		1140	43	2771	4656	43	26134
RELNEALEL		3000	15	30	525	1.1	3337
NEALELKDA		1925	3887	27585	4270	1582	129
LELKDAQAG		451	18706	3659	17293	30	1989

HLA-B44 SUPERTYPE							
Sequence	SEQ ID NO.	B*1801	B*4001	B*4002	B*4402	B*4403	B*4501
MEEPQSDPSV		12157	3802	16536	1927	816	175
VEPPLSQETF		814	>37209.3	21732	406	525	>24019.61
QETFSDLWKL		736	199	255	39	14	901
IEQWFTEDPG		151	1250	2114	5595	142	197
DEAPRMPEAA		121	3941	8444	2594	1037	100
HERCSDSDGL		139	171	61	1468	6.0	1723
VEGNLRVEYL		104	481	2565	1963	22	15189
VEYLDDRNTF		0.94	501	37	32	1.4	3601
PEVGSDCTTI		611	4552	248	2293	2046	22487
LEDSSGNLLG		103	531	697	7905	153	19256
FEVRVCACPG		64	2043	4.9	180	0.76	1872
TEEENLRKKG		74966	>37209.3	11858	>23589.74	315	30635
GEPHHELPPG		108	3323	1888	11728	4.4	20
GEYFTLQIRG		108	88	19	2452	3.9	157
RERFEMFREL		83	29	17	17	0.34	422
FEMFRELNEA		127	3207	223	952	2.0	208
QETFSDLWKLL		4158	3366	740	631	168	1218
HERCSDSDGLA		1408	4879	1915	>20956.72	96	186
YEPPEVGSDCT		16872	4529	125	13349	12712	16034
HELPPGSTKRA		6034	3974	3255	47077	189	1472
FEMFRELNEAL		475	17	8.8	748	1.1	1352
NEALELKDAQA		742	6235	5071	>20956.72	949	53
TEDPGPDEAPRM		888	327	893	2053	161	1676
GEPHHELPPGST		6822	24342	4631	6581	252	169
DEAPRMPEAAPPV		427	>48484.85	7258	>2762.76	1376	19
YEPPEVGSDCTTI		8796	2699	1540	>2740.54	253	>20000
RERRDNYV		>73809.52	71554	62	>67647.06	>34517.77	34648
SEIDLILGY		3.0	285	140	4.8	8.5	397
AEIPTRVNY		1691	7826	5443	333	23	1286
AEMGKFKFSY		1517	2941	622	146	28	283
DEIGVIDLY		11	>114285.71	>77272.73	707	212	>49000
AEMGKFKYSF		155	113	3.8	18	31	186
SEAIHTFQY		25	2895	1802	18	16	1078
SEAIYTFQF		5.7	967	39	4.8	20	293
AEGIVTGQY		7176	6462	1528	255	12	418
HETTYNSI		1644	251	336	616	23959	6608
GELSYLNV		>24800	4856	100	19013	23735	784
YEDTGKTI		13997	794	83	7911	2177	49000
YENDIEKKI		30992	1156	145	1725	371	

TABLE 23

HLA-DQ SUPERTYPES

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
AAAKAAAAAAYAA		13	Artificial sequence			A
(44)YAAAAAAKAAA		13	Artificial sequence			A
AAFAAAKTAAAFA		13	Artificial sequence			A
YAAFAAAKTAAAFA		14	Artificial sequence			A
YAAFAAAKTAAAFA		14	Artificial sequence			
AHAAHAAHAAHAAHAA		16	HA			A
VLERYLLEAKEAENI		15	Human	EPO	11	
VPDTKVNFYAWKRME		15	Human	EPO	41	
WKRMEVGQQAVEVWQ		15	Human	EPO	51	
VGQQAVEVWQGLALL		15	Human	EPO	56	
VEVWQGLALLSEAVL		15	Human	EPO	61	
GLALLSEAVLRGQAL		15	Human	EPO	66	
SEAVLRGQALLVNSS		15	Human	EPO	71	
RGQALLVNSSQPWEP		15	Human	EPO	76	
LQLHVDKAVSGLRSL		15	Human	EPO	91	
KEAISPPDAASAAPL		15	Human	EPO	116	
PPDAASAAPLRTITA		15	Human	EPO	121	
SAAPLRTITADTFRK		15	Human	EPO	126	
EAENITTGTAEHTSL		15	Human	EPO	21	A
RLFDNASLRAHRLHQ		15	Human	Growth hormone	8	
QLAFDTYQEFEEAYI		15	Human	Growth hormone	22	
ISLLLIQSWLEPVQF		15	Human	Growth hormone	78	
NSLVYGASDSNVYDL		15	Human	Growth hormone	99	
SDSNVYDLLKDLEEG		15	Human	Growth hormone	106	
KIFGSLAFLPESFDGDPA		18	Human	Her2/neu	369	
CLKDRRNFDIPEEIK		15	Human	IFN-B	31	
QLQQFQKEDAAVTIY		15	Human	IFN-B	46	
QKEDAAVTIYEMLQN		15	Human	IFN-B	51	
STGWNETIVENLLAN		15	Human	IFN-B	76	
ETIVENLLANVYHQR		15	Human	IFN-B	81	
KEDSHCAWTIVRVEI		15	Human	IFN-B	136	
MSYNLLGFLQRSSNT		15	Human	IFN-B	1	A
QHLCGSHLVEALYLV		15	Human	Insulin beta chain	4	
GSHLVEALYLVCGER		15	Human	Insulin beta chain	8	
GSDLVEALYLVCGER		15	Human	Insulin beta chain	8	A
VEALYLVCGERGFLY		15	Human	Insulin	12	A

HLA-DQ SUPERTYPES						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
VEALYLVTGERGFFY		15	Human	beta chain Insulin	12	A
IDVWLGGLAENFLPY		15	Human	beta chain thyroid	632	
IDVWLGGLAYNFLPY		15	Human	perox thyroid	632	A
IDVWLGGLALNFLPY		15	Human	perox thyroid	632	A
IDVWLGGLASNFLPY		15	Human	perox thyroid	632	A
IDVWLGGLAKNFLPY		15	Human	perox thyroid	632	A
IDVWLGGLADNFLPY		15	Human	perox thyroid	632	A
IDVYLGGLAENFLPY		15	Human	perox thyroid	632	A
IDVLLGGLAENFLPY		15	Human	perox thyroid	632	A
IDVSLGGLAENFLPY		15	Human	perox thyroid	632	A
IDVKLGGLAENFLPY		15	Human	perox thyroid	632	A
IDVDLGGLAENFLPY		15	Human	perox thyroid	632	A
IDVWLGGLAENYLPY		15	Human	perox thyroid	632	A
IDVWLGGLAENVLPY		15	Human	perox thyroid	632	A
IDVWLGGLAENSLPY		15	Human	perox thyroid	632	A
IDVWLGGLAENKLPY		15	Human	perox thyroid	632	A
IDVWLGGLAENDLPY		15	Human	perox thyroid	632	A
IYVWLGGLAENFLPY		15	Human	perox thyroid	632	A
ILVWLGGLAENFLPY		15	Human	perox thyroid	632	A
ISVWLGGLAENFLPY		15	Human	perox thyroid	632	A
IKVWLGGLAENFLPY		15	Human	perox thyroid	632	A
IEVWLGGLAENFLPY		15	Human	perox thyroid	632	A
IDVWLGGLAENFLPF		15	Human	perox thyroid	632	A
IDVWLGGLAENFLPL		15	Human	perox thyroid	632	A
IDVWLGGLAENFLPS		15	Human	perox thyroid	632	A
IDVWLGGLAENFLPK		15	Human	perox thyroid	632	A
IDVWLGGLAENFLPD		15	Human	perox thyroid	632	A

HLA-DQ SUPERTYPES						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
IDVWLGGLAENFYPY		15	Human	perox thyroid	632	A
IDVWLGGLAENFVPY		15	Human	perox thyroid	632	A
IDVWLGGLAENFSPY		15	Human	perox thyroid	632	A
IDVWLGGLAENFKPY		15	Human	perox thyroid	632	A
IDVWLGGLAENFDPY		15	Human	perox thyroid	632	A
IDVWLGGLAEYFLPY		15	Human	perox thyroid	632	A
IDVWLGGLAELFLPY		15	Human	perox thyroid	632	A
IDVWLGGLAESFLPY		15	Human	perox thyroid	632	A
IDVWLGGLAEKFLPY		15	Human	perox thyroid	632	A
IDVWLGGLAEDFLPY		15	Human	perox thyroid	632	A
IDVWLGGLAEQFLPY		15	Human	perox thyroid	632	A
IDVWLGGLYENFLPY		15	Human	perox thyroid	632	A
IDVWLGGLLENFLPY		15	Human	perox thyroid	632	A
IDVWLGGLSENFLPY		15	Human	perox thyroid	632	A
IDVWLGGLKENFLPY		15	Human	perox thyroid	632	A
IDVWLGGLDENFLPY		15	Human	perox thyroid	632	A
IDVWLGGYAENFLPY		15	Human	perox thyroid	632	A
IDVWLGGVAENFLPY		15	Human	perox thyroid	632	A
IDVWLGGSAENFLPY		15	Human	perox thyroid	632	A
IDVWLGGKAENFLPY		15	Human	perox thyroid	632	A
IDVWLGGDAENFLPY		15	Human	perox thyroid	632	A
IDVWLGYLAENFLPY		15	Human	perox thyroid	632	A
IDVWLGLLAENFLPY		15	Human	perox thyroid	632	A
IDVWLGSLAENFLPY		15	Human	perox thyroid	632	A
IDVWLGKLAENFLPY		15	Human	perox thyroid	632	A
IDVWLGDLAENFLPY		15	Human	perox thyroid	632	A
IDVWLYGLAENFLPY		15	Human	perox thyroid	632	A

HLA-DQ SUPERTYPES						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
IDVWLLGLAENFLPY		15	Human	thyroid perox	632	A
IDVWLSGLAENFLPY		15	Human	thyroid perox	632	A
IDVWLKGLAENFLPY		15	Human	thyroid perox	632	A
IDVWLDGLAENFLPY		15	Human	thyroid perox	632	A
IDVWYGGLAENFLPY		15	Human	thyroid perox	632	A
IDVWVGGLAENFLPY		15	Human	thyroid perox	632	A
IDVWSGGLAENFLPY		15	Human	thyroid perox	632	A
IDVWKGGLAENFLPY		15	Human	thyroid perox	632	A
IDVWDGGLAENFLPY		15	Human	thyroid perox	632	A
IDYWLGGLAENFLPY		15	Human	thyroid perox	632	A
IDLWLGGLAENFLPY		15	Human	thyroid perox	632	A
IDSWLGGLAENFLPY		15	Human	thyroid perox	632	A
IDKWLGGLAENFLPY		15	Human	thyroid perox	632	A
IDDWLGGLAENFLPY		15	Human	thyroid perox	632	A
IDVWLGGLAENFLYY		15	Human	thyroid perox	632	A
IDVWLGGLAENFLLY		15	Human	thyroid perox	632	A
IDVWLGGLAENFLSY		15	Human	thyroid perox	632	A
IDVWLGGLAENFLKY		15	Human	thyroid perox	632	A
IDVWLGGLAENFLDY		15	Human	thyroid perox	632	A
YDVWLGGLAENFLPY		15	Human	thyroid perox	632	A
LDVWLGGLAENFLPY		15	Human	thyroid perox	632	A
SDVWLGGLAENFLPY		15	Human	thyroid perox	632	A
KDVWLGGLAENFLPY		15	Human	thyroid perox	632	A
DDVWLGGLAENFLPY		15	Human	thyroid perox	632	A

TABLE 24

HLA-DQ SUPERTYPES				
Sequence	SEQ ID NO.	DQB1*030 1	DQB1*030 2	DQB1*020 1
AAAKAAAAAAYAA		424		
(44)YAAAAAAKAAA		26		
AAFAAAKTAAAFA		49		
YAAFAAAKTAAAFA		36		
YAAFAAAKTAAAFA		39		
AHAAHAAHAAHAAHAA		58		
VLERYLLEAKEAENI		10932	309	5389
VPDTKVNFYAWKRME		730	>46666.67	>147058.82
WKRMEVGQQAVEVWQ		13666	12146	159
VGQQAVEVWQGLALL		1807	4407	838
VEVWQGLALLSEAVL		19	14	98
GLALLSEAVLRGQAL		107	16963	6742
SEAVLRGQALLVNSS		55	36395	9755
RGQALLVNSSQPWEP		302	14393	13362
LQLHVDKAVSGLRSL		88	7842	7590
KEAISPPDAASAAPL		458	960	7287
PPDAASAAPLRTITA		20	3869	3631
SAAPLRTITADTFRK		301	>46666.67	1100
EAENITTGTAEHTSL		316	8300	
RLFDNASLRAHRLHQ		996	>36206.9	11766
QLAFDTYQEFEEAYI		>89285.71	673	35
ISLLLIQSWLEPVQF		>89285.71	562	5234
NSLVYGASDSNVYDL		14164	8337	731
SDSNVYDLLKDLEEG		>89285.71	4136	503
KIFGSLAFLPESFDGDPA		320		
CLKDRRNFDIPEEIK		19365	208	774
QLQQFQKEDAAVTIY		26205	579	2145
QKEDAAVTIYEMLQN		515	153	1685
STGWNETIVENLLAN		47081	5041	322
ETIVENLLANVYHQR		>92592.59	>75000	344
KEDSHCAWTIVRVEI		4102	2123	465
MSYNLLGFLQRSSNT		724	>51219.51	
QHLCGSHLVEALYLV		2553	8413	359
GSHLVEALYLVCGER		>89285.71	2491	677
GSDLVEALYLVCGER		>89285.71	806	
VEALYLVCGERGFLY		27334	514	
VEALYLVTGERGFFY		20021	564	
IDVWLGGLAENFLPY		204	138	13
IDVWLGGLAYNFLPY		85	358	63
IDVWLGGLALNFLPY		49	457	52
IDVWLGGLASNFLPY		175	1251	40
IDVWLGGLAKNFLPY		170	10247	>4166.67
IDVWLGGLADNFLPY		296	1762	12
IDVYLGGLAENFLPY		161	186	30

HLA-DQ SUPERTYPES				
Sequence	SEQ ID NO.	DQB1*030 1	DQB1*030 2	DQB1*020 1
IDVLLGGLAENFLPY		166	437	27
IDVSLGGLAENFLPY		188	277	48
IDVKLGGLAENFLPY		724	5511	41
IDVDLGGLAENFLPY		218	73	17
IDVWLGGLAENYLPY		223	110	19
IDVWLGGLAENVLPY		84	82	15
IDVWLGGLAENSLPY		116	125	25
IDVWLGGLAENKLPY		353	5189	51
IDVWLGGLAENDLPY		240	60	22
IYVWLGGLAENFLPY		170	237	13
ILVWLGGLAENFLPY		216	147	10.0
ISVWLGGLAENFLPY		132	286	18
IKVWLGGLAENFLPY		180	220	37
IEVWLGGLAENFLPY		158	145	23
IDVWLGGLAENFLPF		111	177	3.6
IDVWLGGLAENFLPL		182	114	17
IDVWLGGLAENFLPS		134	249	27
IDVWLGGLAENFLPK		261	231	23
IDVWLGGLAENFLPD		115	91	20
IDVWLGGLAENFYPY		324	203	37
IDVWLGGLAENFVPY		346	272	12
IDVWLGGLAENFSPY		131	193	47
IDVWLGGLAENFKPY		195	262	310
IDVWLGGLAENFDPY		364	90	32
IDVWLGGLAEYFLPY		151	88	14
IDVWLGGLAELFLPY		107	81	22
IDVWLGGLAESFLPY		60	64	49
IDVWLGGLAEKFLPY		68	112	66
IDVWLGGLAEDFLPY		357	120	23
IDVWLGGLAEQFLPY		167	123	9.7
IDVWLGGLYENFLPY		912	697	6.4
IDVWLGGLLENFLPY		810	1734	58
IDVWLGGLSENFLPY		242	1348	37
IDVWLGGLKENFLPY		15907	>2800	25
IDVWLGGLDENFLPY		>19230.77	637	18
IDVWLGGYAENFLPY		900	492	39
IDVWLGGVAENFLPY		982	327	75
IDVWLGGSAENFLPY		427	755	166
IDVWLGGKAENFLPY		517	633	398
IDVWLGGDAENFLPY		11114	2074	11
IDVWLGYLAENFLPY		15215	1121	31
IDVWLGLLAENFLPY		2986	180	39
IDVWLGSLAENFLPY		654	278	72
IDVWLGKLAENFLPY		2333	20023	81
IDVWLGDLAENFLPY		>44642.86	370	18
IDVWLYGLAENFLPY		2171	442	18

HLA-DQ SUPERTYPES				
Sequence	SEQ ID NO.	DQB1*0301	DQB1*0302	DQB1*0201
IDVWLLGLAENFLPY		4903	455	47
IDVWLSGLAENFLPY		3043	373	98
IDVWLKGLAENFLPY		41667	1115	55
IDVWLDGLAENFLPY		13325	357	43
IDVWYGGLAENFLPY		375	224	43
IDVWVGGLAENFLPY		128	158	14
IDVWSGGLAENFLPY		451	128	15
IDVWKGGLAENFLPY		256	346	41
IDVWDGGLAENFLPY		2086	299	112
IDYWLGGLAENFLPY		503	342	49
IDLWLGGLAENFLPY		1292	661	25
IDSWLGGLAENFLPY		508	276	35
IDKWLGGLAENFLPY		579	534	62
IDDWLGGLAENFLPY		219	101	85
IDVWLGGLAENFLYY		341	387	154
IDVWLGGLAENFLLY		649	491	52
IDVWLGGLAENFLSY		425	676	54
IDVWLGGLAENFLKY		2266	995	111
IDVWLGGLAENFLDY		371	149	49
YDVWLGGLAENFLPY		482	214	59
LDVWLGGLAENFLPY		180	216	29
SDVWLGGLAENFLPY		154	232	19
KDVWLGGLAENFLPY		348	254	54
DDVWLGGLAENFLPY		241	158	48

TABLE 25

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
AC-NPTKHKWEAAHVAEQLAA	18	A2	MHC derived	Unknown		
DDYVKQYTKQYTKQNTLKK	19	Artificial sequence				
AAAKAAAAAAAYAA	13	Artificial sequence				A
AC-AAAKAAAAAAYAA	13	Artificial sequence				A
(20)AYA(20)A(20)A(20)K(20)A(20)	13	Artificial sequence				A
AC-AAAKATAAAAYAA	13	Artificial sequence				A
AC-AAAKAAAAAAFAA	13	Artificial sequence				A
AC-AAAKATAAAA(10)AA	13	Artificial sequence				A
AC-AAAKATAAAA(23)AA	13	Artificial sequence				A
AAKAAAAAAA(10)AA	13	Artificial sequence				A
AAYAAAATAKAAA	13	Artificial sequence				A
AALAAAAAAKAAA	13	Artificial sequence				A
AAEAAAATAKAAA	13	Artificial sequence				A
AAYJJAAAAKAAA	13	Artificial sequence				A
AAYAAAAJJKAAA	13	Artificial sequence				A
AFLRAAAAAAFAA	13	Artificial sequence				A
AFLRQAAAAAFAAY	14	Artificial sequence				A
AAFAAAKTAAAFA	13	Artificial sequence				A
YAAFAAAKTAAAFA	14	Artificial sequence				A
AALKATAAAAAAA	13	Artificial sequence				A
YAR(15)ASQTTLKAKT	14	Artificial sequence				
YARF(33)QTTLKAKT	14	Artificial sequence				
PKYFKQRILKFAT	13	Artificial sequence				A
PKYFKQGFLKGAT	13	Artificial sequence				A
PKYGKQIDLKGAT	13	Artificial sequence				A
AAFFFFFGGGGGA	13	Artificial sequence				
AADFFFFFFFFDA	13	Artificial sequence				
AAKGIKIGFGIFA	13	Artificial sequence				
AAFIFIGGGKIKA	13	Artificial sequence				
AAKIFIGFFIDGA	13	Artificial sequence				

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
AAFIGFGKIKFIA		13	Artificial sequence			
AAKIGFGIKIGFA		13	Artificial sequence			
AAFKIGKFGIFFA		13	Artificial sequence			
AADDDDDDDDDDA		13	Artificial sequence			
(43)AAIGFFFFKKGIA		14	Artificial sequence			
(43)AAFFGIFKIGKFA		14	Artificial sequence			
(43)AADFGIFIDFIIA		14	Artificial sequence			
(43)AAIGGIFIFKKDA		14	Artificial sequence			
(43)AAFIGFGKIKFIA		13	Artificial sequence			
(43)AAKIGFGIKIGFA		13	Artificial sequence			
(43)AAFKIGKFGIFFA		13	Artificial sequence			
AAAKAAAAAAAAF		13	Artificial sequence			
AAAKAAAAAAAFA		13	Artificial sequence			
AAAKAAAAAAFAA		13	Artificial sequence			
AAAKAAAAFAAAA		13	Artificial sequence			
FAAAAAAAAAAAA		13	Artificial sequence			
AAAAAAAAAAAAN		13	Artificial sequence			
AAAAAAAAAAANA		13	Artificial sequence			
AAANAAAAAAAAA		13	Artificial sequence			
AAAAAAAAAAAAS		13	Artificial sequence			
AAAAASAAAAAAA		13	Artificial sequence			
ASAAAAAAAAAAA		13	Artificial sequence			
AFAAAKTAA		9	Artificial sequence			
YARFLALTTLRARA		14	Artificial sequence			A
YAR(15A)SQTTLKAKT		14	Artificial sequence			A
YAR(15A)RQTTLKAA A		14	Artificial sequence			A
(15A)RQTTLKAAA		11	Artificial sequence			A
(16A)RQTTLKAAA		11	Artificial sequence			A
(46)AAKTAAAFA		10	Artificial sequence			
(39)AAAATKAAA		10	Artificial sequence			
(52)AAAATKAAAA		11	Artificial sequence			

HLA-DR SUPERTYPE					
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
(55)AAAATKAAAA		11	Artificial sequence			
A(14)AAAKTAAA		10	Artificial sequence			
AA(14)A(35)ATKAAA A		12	Artificial sequence			
AA(14)AA(36)TKAAA A		12	Artificial sequence			
AFAAAKTAA(72)		10	Artificial sequence			
(49)AAAKT(64)AAA		10	Artificial sequence			
(49)AAAKTA(64)AA		10	Artificial sequence			
HQAISPRTLNGPGPGS PAIF		20	Artificial sequence			
YAAFAAAKTAAAFA		14	Artificial sequence			
TEGRCLHYTVDKSKP K		16	Bee Venom		103	
AWVAWRNRCK		0	Chicken	HEL	107	
IVSDGNGMNAWVAW RNRC		18	Chicken	HEL	98	
PHHTALRQAILSWGE LMTLA		20	DPw4 binder			
WMYYHGQRHSDEHH H		15	EBV	LMP	183	
YIVMSDWTGGA		15	EBV	LMP	41	
AHAAHAAHAAHAAH AA		16	HA			A
MDIDPYKEFGATVEL LSFLPSDFFP		25	HBV	core	1	
GMLPVCPLIPGSSTTS TGP		19	HBV	env	102	
LGFFPDHQLDPAFRA NT		17	HBV	env	11	
GYKVLVLNPSV		11	HCV	NS3	1248	
LMAFTAAVTS		10	HCV	NS4	1790	
TFALWRVSAEEY		12	HCV	NS5	2079	
ALWRVSAEEY		10	HCV	NS5	2081	
EEYVEIRQVGDFH		13	HCV	NS5	2088	
VGGVYLLPRRGPRLG V		16	HCV			
VGGAYLLPRRGPRLG V		16	HCV			A
VGGVALLPRRGPRLG V		16	HCV			A
VGGVYALPRRGPRLG V		16	HCV			A
VGGVYLAPRRGPRLG V		16	HCV			A
VGGVYLLARRGPRLG V		16	HCV			A
VGGVYLLPARGPRLG V		16	HCV			A
VGGVYLLRRAGPRLG V		16	HCV			A
GAPLGGAARALAHGV		15	HCV			
GAALGGAARALAHG V		15	HCV			A

HLA-DR SUPERTYPE					
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
GAPLAGAARALAHGV		15	HCV			A
GAPLGAAARALAHGV		15	HCV			A
GAPLGGLARALAHGV		15	HCV			A
GAPLGGALRALAHGV		15	HCV			A
GAPLGGAAAALAHGV		15	HCV			A
GAPLGGAARLLAHGV		15	HCV			A
GAPLGGAARAAAHGV		15	HCV			A
GAPLGGAARALAAGV		15	HCV			A
FPDWQNYTPGPGTRF		15	HIV	NEF	200	
RFPLTFGWCFKLVPV		15	HIV	NEF	216	
RQDILDLWVYHTQGY		15	HIV	NEF	182	
RQEILDLWVYHTQGF		15	HIV	NEF	182	
LSHFLKEKGGLEGLI		15	HIV	NEF	114	
LSFFLKEKGGLDGLI		15	HIV	NEF	114	
LEPWNHPGSQPKTACT		16	HIV	TAT	11	
QVCFITKGLGISYGR		15	HIV	TAT	38	
QLCFLKKGLGISYGR		15	HIV	TAT	38	
PPEESFRFGEEKTTPS		16	HIV1	gp	81	
CIVYRDGNPYAVCDK		15	HPV	E6	58	
HYCYSLYGTTLEQQY		15	HPV	E6	85	
CYSLYGTTLEQQYNK		15	HPV	E6	87	
NTSLQDIEITCVYCK		15	HPV	E6	22	
VFEFAFKDLFVVYRD		15	HPV	E6	44	
EFAFKDLFVVYRDSI		15	HPV	E6	46	
DLFVVYRDSIPHAAC		15	HPV	E6	51	
FVVYRDSIPHAACHK		15	HPV	E6	53	
NTGLYNLLIRCLRCQ		15	HPV	E6	95	
IRCLRCQKPLNPAEK		15	HPV	E6	103	
PRKLHELSSALEIPY		15	HPV	E6	9	
EIPYDELRLNCVYCK		15	HPV	E6	20	
TEVLDFAFTDLTIVY		15	HPV	E6	40	
VLDFAFTDLTIVYRD		15	HPV	E6	42	
DFAFTDLTIVYRDDT		15	HPV	E6	44	
TIVYRDDTPHGVCTK		15	HPV	E6	51	
WYRYSVYGTTLEKLT		15	HPV	E6	78	
ETTIHNIELQCVECK		15	HPV	E6	20	
SEVYDFAFADLTVVY		15	HPV	E6	40	
VYDFAFADLTVVYRE		15	HPV	E6	42	
DFAFADLTVVYREGN		15	HPV	E6	44	
TVVYREGNPFGICKL		15	HPV	E6	51	
GNPFGICKLCLRFLS		15	HPV	E6	57	
NYSVYGNTLEQTVKK		15	HPV	E6	80	
KKPLNEILIRCIICQ		15	HPV	E6	93	
NEILIRCIICQRPLC		15	HPV	E6	97	
IRCIICQRPLCPQEK		15	HPV	E6	101	

HLA-DR SUPERTYPE					
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
CIVYRDCIAYAACHK		15	HPV	E6	53	
NTELYNLLIRCLRCQ		15	HPV	E6	95	
IRCLRCQKPLNPAEK		15	HPV	E6	103	
REVYKFLFTDLRIVY		15	HPV	E6	40	
RIVYRDNNPYGVCIM		15	HPV	E6	51	
NNPYGVCIMCLRFLS		15	HPV	E6	57	
EERVKKPLSEITIRC		15	HPV	E6	89	
IRCIICQTPLCPEEK		15	HPV	E6	101	
EIPLIDLRLSCVYCK		15	HPV	E6	23	
SCVYCKKELTRAEVY		15	HPV	E6	32	
VCLLFYSKVRKYRYY		15	HPV	E6	68	
YYDYSVYGATLESIT		15	HPV	E6	81	
IRCYRCQSPLTPEEK		15	HPV	E6	104	
VYDFVFADLRIVYRD		15	HPV	E6	42	
DFVFADLRIVYRDGN		15	HPV	E6	44	
RIVYRDGNPFAVCKV		15	HPV	E6	51	
GNPFAVCKVCLRLLS		15	HPV	E6	57	
KKCLNEILIRCIICQ		15	HPV	E6	93	
NEILIRCIICQRPLC		15	HPV	E6	97	
RTAMFQDPQERPRKL		15	HPV	E6	5	
LFVVYRDSIPHAACH		15	HPV	E6	52	
LTIVYRDDTPHGVCT		15	HPV	E6	50	
LCIVYRDCIAYAACH		15	HPV	E6	52	
YKFLFTDLRIVYRDN		15	HPV	E6	43	
YNFACTELKLVYRDD		15	HPV	E6	46	
LKLVYRDDFPYAVCR		15	HPV	E6	53	
YDFVFADLRIVYRDG		15	HPV	E6	43	
LRIVYRDGNPFAVCK		15	HPV	E6	50	
HEYMLDLQPETTDLY		15	HPV	E7	9	
TLRLCVQSTHVDIRT		15	HPV	E7	64	
IRTLEDLLMGTLGIV		15	HPV	E7	76	
LEDLLMGTLGIVCPI		15	HPV	E7	79	
DLLMGTLGIVCPICS		15	HPV	E7	81	
KATLQDIVLHLEPQN		15	HPV	E7	5	
IDGVNHQHLPARRAE		15	HPV	E7	41	
LRAFQQLFLNTLSFV		15	HPV	E7	83	
FQQLFLNTLSFVCPW		15	HPV	E7	86	
QDYVLDLQPEATDLH		15	HPV	E7	9	
DIRILQELLMGSFGI		15	HPV	E7	75	
IRILQELLMGSFGIV		15	HPV	E7	76	
ELLMGSFGIVCPNCS		15	HPV	E7	81	
KEYVLDLYPEPTDLY		15	HPV	E7	9	
LRTIQQLLMGTVNIV		15	HPV	E7	76	
IQQLLMGTVNIVCPT		15	HPV	E7	79	
QLLMGTVNIVCPTCA		15	HPV	E7	81	
RETLQEIVLHLEPQN		15	HPV	E7	5	

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
LRTLQQLFLSTLSFV		15	HPV	E7	84	
LQQLFLSTLSFVCPW		15	HPV	E7	87	
KDYILDLQPETTDLH		15	HPV	E7	9	
LRTLQQMLLGTLQVV		15	HPV	E7	78	
LQQMLLGTLQVVCPG		15	HPV	E7	81	
QMLLGTLQVVCPGCA		15	HPV	E7	83	
VPTLQDVVLELTPQT		15	HPV	E7	5	
LQDVVLELTPQTEID		15	HPV	E7	8	
QDVVLELTPQTEIDL		15	HPV	E7	9	
CKFVVQLDIQSTKED		15	HPV	E7	68	
VVQLDIQSTKEDLRV		15	HPV	E7	71	
DLRVVQQLLMGALTV		15	HPV	E7	82	
LRVVQQLLMGALTVT		15	HPV	E7	83	
VQQLLMGALTVTCPL		15	HPV	E7	86	
QQLLMGALTVTCPLC		15	HPV	E7	87	
QLLMGALTVTCPLCA		15	HPV	E7	88	
REYILDLHPEPTDLF		15	HPV	E7	9	
TCCYTCGTTVRLCIN		15	HPV	E7	57	
VRTLQQLLMGTCTIV		15	HPV	E7	77	
LQQLLMGTCTIVCPS		15	HPV	E7	80	
MLDLQPETTDLYCYE		15	HPV	E7	12	
VLDLYPEPTDLYCYE		15	HPV	E7	12	
LREYILDLHPEPTDL		15	HPV	E7	8	
HIEFTPTRTDTYACRV		16	Human	B2-μglobulin	67	
LWWVNNESLPVSPRL		15	Human	CEA	177	A
YEEYVRFDSDVGE		13	Human	DRB and CD4 peptide		
EEYVRFDSDVGE		12	Human	DRB and CD4 peptide		
APPRLICDSRVLERY		15	Human	EPO	1	
ICDSRVLERYLLEAK		15	Human	EPO	6	
VLERYLLEAKEAENI		15	Human	EPO	11	
EHCSLNENITVPDTK		15	Human	EPO	31	
NENITVPDTKVNFYA		15	Human	EPO	36	
VPDTKVNFYAWKRME		15	Human	EPO	41	
VNFYAWKRMEVGQQA		15	Human	EPO	46	
WKRMEVGQQAVEVWQ		15	Human	EPO	51	
VGQQAVEVWQGLALL		15	Human	EPO	56	
VEVWQGLALLSEAVL		15	Human	EPO	61	
GLALLSEAVLRGQAL		15	Human	EPO	66	
SEAVLRGQALLVNSS		15	Human	EPO	71	
RGQALLVNSSQPWEP		15	Human	EPO	76	
LVNSSQPWEPLQLHV		15	Human	EPO	81	
QPWEPLQLHVDKAVS		15	Human	EPO	86	
LQLHVDKAVSGLRSL		15	Human	EPO	91	

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
DKAVSGLRSLTTLLR		15	Human	EPO	96	
GLRSLTTLLRALGAQ		15	Human	EPO	101	
TTLLRALGAQKEAIS		15	Human	EPO	106	
ALGAQKEAISPPDAA		15	Human	EPO	111	
KEAISPPDAASAAPL		15	Human	EPO	116	
PPDAASAAPLRTITA		15	Human	EPO	121	
SAAPLRTITADTFRK		15	Human	EPO	126	
RTITADTFRKLFRVY		15	Human	EPO	131	
DTFRKLFRVYSNFLR		15	Human	EPO	136	
LFRVYSNFLRGKLKL		15	Human	EPO	141	
SNFLRGKLKLYTGEA		15	Human	EPO	146	
KLKLYTGEACRTGDR		15	Human	EPO	152	
APPRLITDSRVLERY		15	Human	EPO	1	A
ITDSRVLERYLLEAK		15	Human	EPO	6	A
EHTSLNENITVPDTK		15	Human	EPO	31	A
KLKLYTGEATRTGDR		15	Human	EPO	152	A
PQPFRPQQPYPQ		12	Human	gliadin		
PFRPQQPYPQ		10	Human	gliadin		
PQPFRPQQPYP		11	Human	gliadin		
PQPFRPQQP		9	Human	gliadin		
KQPFRPQQPYPQ		12	Human	gliadin		
PKPFRPQQPYPQ		12	Human	gliadin		
PQPFKPQQPYPQ		12	Human	gliadin		
PQPFRKQQPYPQ		12	Human	gliadin		
PQPFRPQKPYPQ		12	Human	gliadin		
PQPFRPQQPKPQ		12	Human	gliadin		
PQPFRPQQPYKQ		12	Human	gliadin		
PQPFRPQQPYPK		12	Human	gliadin		
QFLGQQQPFPPQ		12	Human	gliadin		
FLGQQQPFPPQ		11	Human	gliadin		
LGQQQPFPPQ		10	Human	gliadin		
QFLGQQQPFPP		11	Human	gliadin		
QFLGQQQPF		9	Human	gliadin		
IRNLALQTLPAMCNVY		16	Human	gliadin		
NLALQTLPAMCNVY		14	Human	gliadin		
LALQTLPAMCNVY		13	Human	gliadin		
IRNLALQTLPAM		12	Human	gliadin		
IRNLALQTLP		10	Human	gliadin		
EGDAFELTVSCQGGLPK		17	Human	gp100	506	
ESTGMTPEKVPVSEVMGT		18	Human	gp100	370	
FPTIPLSRLFDNASL		15	Human	Growth hormone	1	
RLFDNASLRAHRLHQ		15	Human	Growth hormone	8	
LRAHRLHQLAFDTYQ		15	Human	Growth hormone	15	

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
QLAFDTYQEFEEAYI		15	Human	Growth hormone	22	
QEFEEAYIPKEQKYS		15	Human	Growth hormone	29	
IPKEQKYSFLQNPQT		15	Human	Growth hormone	36	
SFLQNPQTSLCFSES		15	Human	Growth hormone	43	
TSLCFSESIPTPSNR		15	Human	Growth hormone	50	
REETQQKSNLELLRI		15	Human	Growth hormone	64	
SNLELLRISLLLIQS		15	Human	Growth hormone	71	
ISLLLIQSWLEPVQF		15	Human	Growth hormone	78	
SWLEPVQFLRSVFAN		15	Human	Growth hormone	85	
FLRSVFANSLVYGAS		15	Human	Growth hormone	92	
NSLVYGASDSNVYDL		15	Human	Growth hormone	99	
SDSNVYDLLKDLEEG		15	Human	Growth hormone	106	
GIQTLMGRLEDGSPR		15	Human	Growth hormone	120	
RLEDGSPRTGQIFKQ		15	Human	Growth hormone	127	
RTGQIFKQTYSKFDT		15	Human	Growth hormone	134	
QTYSKFDTNSHNDDA		15	Human	Growth hormone	141	
TNSHNDDALLKNYGL		15	Human	Growth hormone	148	
ALLKNYGLLYCFRKD		15	Human	Growth hormone	155	
DMDKVETFLRIVQCR		15	Human	Growth hormone	169	
FLRIVQCRSVEGSCGF		16	Human	Growth hormone	176	
FPTIPLSRLFDNAML		15	Human	Growth hormone	1	A
RLFDNAMLRAHRLHQ		15	Human	Growth hormone	8	A
QLAFDTYQEFEQNPQ		15	Human	Growth hormone	22	A
SFLQNPQTSLCCFRK		15	Human	Growth hormone	43	A
SNLELLRICLLLIQS		15	Human	Growth hormone	71	A
ICLLLIQSWLEPVQF		15	Human	Growth hormone	78	A
NSLVYGASDSNIYDL		15	Human	Growth hormone	99	A
SDSNIYDLLKDLEEG		15	Human	Growth hormone	106	A
DKVETFLRIVQCCGF		15	Human	Growth hormone	169	A
SFLQNPQTSLTFSES		15	Human	Growth hormone	43	A
TSLTFSESIPTPSNR		15	Human	Growth hormone	50	A

HLA-DR SUPERTYPE					
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
ALLKNYGLLYTFRKD		15	Human	Growth hormone	155	A
LLYTFRKDMDKVETF		15	Human	Growth hormone	162	A
DMDKVETFLRIVQTR		15	Human	Growth hormone	169	A
FLRIVQTRSVEGSTGF		16	Human	Growth hormone	176	A
HLDMLRHLYQGCQVV		15	Human	Her2/neu	42	
RLRIVRGTQLFEDNYAL		17	Human	Her2/neu	98	
GVGSPYVSRLLGICL		15	Human	Her2/neu	776	
TLERPKTLSPGKNGV		15	Human	Her2/neu	1166	
KIFGSLAFLPESFDGDPA		18	Human	Her2/neu	369	
ELVSEFSRMARDPQ		14	Human	Her2/neu	971	
GEALSTLVLNRLKVG		15	Human	HSP60	280	
AYVLLSEKKISSIQS		15	Human	HSP60	242	
VASLLTTAEVVVTEI		15	Human	HSP60	535	
KCEFQDAYVILLSEKK		16	Human	HSP60	236	
ALSTLVLNRLKVGLQ		15	Human	HSP60	282	
MSYNLLGFLQRSSNC		15	Human	IFN-B	1	
LGFLQRSSNCQCQKL		15	Human	IFN-B	6	
RSSNCQCQKLLWQLN		15	Human	IFN-B	11	
QCQKLLWQLNGRLEY		15	Human	IFN-B	16	
LWQLNGRLEYCLKDR		15	Human	IFN-B	21	
GRLEYCLKDRRNFDI		15	Human	IFN-B	26	
RNFDIPEEIKQLQQF		15	Human	IFN-B	36	
PEEIKQLQQFQKEDA		15	Human	IFN-B	41	
QLQQFQKEDAAVTIY		15	Human	IFN-B	46	
QKEDAAVTIYEMLQN		15	Human	IFN-B	51	
AVTIYEMLQNIFAIF		15	Human	IFN-B	56	
EMLQNIFAIFRQDSS		15	Human	IFN-B	61	
IFAIFRQDSSSTGWN		15	Human	IFN-B	66	
RQDSSSTGWNETIVE		15	Human	IFN-B	71	
STGWNETIVENLLAN		15	Human	IFN-B	76	
ETIVENLLANVYHQR		15	Human	IFN-B	81	
NLLANVYHQRNHLKT		15	Human	IFN-B	86	
VYHQRNHLKTVLEEK		15	Human	IFN-B	91	
LEKEDFTRGKRMSSL		15	Human	IFN-B	106	
FTRGKRMSSLHLKRY		15	Human	IFN-B	111	
RMSSLHLKRYYGRIL		15	Human	IFN-B	116	
HLKRYYGRILHYLKA		15	Human	IFN-B	121	
YGRILHYLKAKEDSH		15	Human	IFN-B	126	
HYLKAKEDSHCAWTI		15	Human	IFN-B	131	
KEDSHCAWTIVRVEI		15	Human	IFN-B	136	
CAWTIVRVEILRNFY		15	Human	IFN-B	141	
VRVEILRNFYVINRL		15	Human	IFN-B	146	
RNFYVINRLTGYLRN		15	Human	IFN-B	152	

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
MSYNLLGFLQRSSNT		15	Human	IFN-B	1	A
LGFLQRSSNTQTQKL		15	Human	IFN-B	6	A
RSSNTQTQKLLWQLN		15	Human	IFN-B	11	A
QTQKLLWQLNGRLEY		15	Human	IFN-B	16	A
LWQLNGRLEYTLKDR		15	Human	IFN-B	21	A
GRLEYTLKDRRNFDI		15	Human	IFN-B	26	A
HYLKAKEDSHTAWTI		15	Human	IFN-B	131	A
KEDSHTAWTIVRVEI		15	Human	IFN-B	136	A
TAWTIVRVEILRNFY		15	Human	IFN-B	141	A
LGFLQRSSNCQSQKL		15	Human	IFN-B	6	A
RSSNCQSQKLLWQLN		15	Human	IFN-B	11	A
QSQKLLWQLNGRLEY		15	Human	IFN-B,	16	A
GIVEQCCTSICSLYQ		15	Human	Insulin alpha chain	1	
TSICSLYQLENYCN		14	Human	Insulin alpha chain	8	
GILEQCCTSICSLYQ		15	Human	Insulin alpha chain	1	A
GIVEQTTTSITSLYQ		15	Human	Insulin alpha chain	1	A
EQTTTSITSLYQLEN		15	Human	Insulin alpha chain	4	A
TSICSLYQLENYCG		14	Human	Insulin alpha chain	8	A
TSITSLYQLENYTN		14	Human	Insulin alpha chain	8	A
TSITSLYQLENYTG		14	Human	Insulin alpha chain	8	A
GIVEQCCCGSHLVEA		15	Human	Insulin alpha-beta		A
SLYQLENYCCGERGF		15	Human	Insulin alpha-beta		A
CCTSICSLYQLENYCC		16	Human	Insulin alpha-beta		A
GSHLVEALYLVCCN		14	Human	Insulin alpha-beta		A
CCGSHLVEALYLVCC		15	Human	Insulin alpha-beta		A
FVNQHLCGSHLVEAL		15	Human	Insulin beta chain	1	
QHLCGSHLVEALYLV		15	Human	Insulin beta chain	4	
GSHLVEALYLVCGER		15	Human	Insulin beta chain	8	
VEALYLVCGERGFFY		15	Human	Insulin beta chain	12	
YLVCGERGFFYTPKT		15	Human	Insulin beta chain	16	
FVNQHLCGSDLVEAL		15	Human	Insulin beta chain	1	A
FVNQHLTGSHLVEAL		15	Human	Insulin beta chain	1	A
QHLTGSHLVEALYLV		15	Human	Insulin beta chain	4	A
GSHLVEALYLVTGER		15	Human	Insulin beta chain	8	A
VEALYLVCGERGSFY		15	Human	Insulin beta chain	12	A

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
VEALYLVCGERGFLY		15	Human	Insulin beta chain	12	A
VEALYLVTGERGFFY		15	Human	Insulin beta chain	12	A
YLVCGERGFLYTPKT		15	Human	Insulin beta chain	16	A
YLVCGERGFFYTDKT		15	Human	Insulin beta chain	16	A
YLVCGERGFFYTKPT		15	Human	Insulin beta chain	16	A
YLVTGERGFFYTPKT		15	Human	Insulin beta chain	16	A
YLVTGERGFFYTDKT		15	Human	Insulin beta chain	16	A
YLVTGERGFFYTKPT		15	Human	Insulin beta chain	16	A
VCGERGFFYTPKTRR		15	Human	Insulin beta chain	18	A
VTGERGFFYTPKTRR		15	Human	Insulin beta chain	18	A
MWDLVLSIALSVGCT		15	Human	Kallikrein2	1	
DLVLSIALSVGCTGA		15	Human	Kallikrein2	3	
HPQWVLTAAHCLKK N		15	Human	Kallikrein2	56	
QWVLTAAHCLKKNS Q		15	Human	Kallikrein2	58	
GQRVPVSHSFPHPLY		15	Human	Kallikrein2	87	
RVPVSHSFPHPLYNM		15	Human	Kallikrein2	89	
PHPLYNMSLLKHQSL		15	Human	Kallikrein2	97	
HPLYNMSLLKHQSLR		15	Human	Kallikrein2	98	
NMSLLKHQSLRPDED		15	Human	Kallikrein2	102	
SHDLMLLRLSEPAKI		15	Human	Kallikrein2	118	
HDLMLLRLSEPAKIT		15	Human	Kallikrein2	119	
PEEFLRPRSLQCVSL		15	Human	Kallikrein2	162	
PRSLQCVSLHLLSND		15	Human	Kallikrein2	168	
NGVLQGITSWGPEPC		15	Human	Kallikrein2	220	
KPAVYTKVVHYRKWI		15	Human	Kallikrein2	239	
LHLLSNDMCARAYSE		15	Human	Kallikrein2	176	
VGNWQYFFPVIFSKA		15	Human	MAGE3	140	
ESEFQAALSRKVAKL		15	Human	MAGE6	102	
IGHLYIFATCLGLSYD GL		18	Human	MAGE6	172	
VGNWQYFFPVIFSKAS DSLQLVFGIELMEVD		31	Human	MAGE6	140	
PAYEKLSAEQSPPPY		15	Human	MART1	102	
RNGYRALMDKSLHV GTQCALTRR		23	Human	MART1	51	
FFKNIVTFFKNIVT		14	Human	MBP		A
YKSAHKGFKGVDAQ GTLSKI		20	Human	MBP	134	
VDAQGTLSKIFKLGG RDSRS		20	Human	MBP	144	
AC-ASQKRPSQRHGSKYL ATAST		23	Human	MBP	1	
ENPVVHFFKNIVTPR		15	Human	MBP	85	

HLA-DR SUPERTYPE					
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
ENPVVAFFKNIVTPR		15	Human	MBP	85	SAAS
ENPVVHAFKNIVTPR		15	Human	MBP	85	SAAS
ENPVVHFFANIVTPR		15	Human	MBP	85	SAAS
ENPVVHFFKNIVTPA		15	Human	MBP	85	SAAS
NPVVHFFKNIVT		12	Human	MBP	86	
HFFKNIVTPRTPPY		14	Human	MBP	90	
NPVVHFFKNIVTPR		14	Human	MBP	86	
LPVPGVLLKEFTVSGN ILTI		20	Human	NY-ESO-1	116	
WITQCFLPVFLAQPPS GQRR		20	Human	NY-ESO-1	161	
DHRQLQLSISSCLQQL SLLM		20	Human	NY-ESO-1	141	
YLAMPFATPMEAELA RRSLA		20	Human	NY-ESO-1	91	
AAPLLLARAASLSLG		15	Human	PAP	3	
APLLLARAASLSLGF		15	Human	PAP	4	
PLLLARAASLSLGFL		15	Human	PAP	5	
SLSLGFLFLLFFWLD		15	Human	PAP	13	
LLFFWLDRSVLAKEL		15	Human	PAP	21	
DRSVLAKELKFVTLV		15	Human	PAP	27	
AKELKFVTLVFRHGD		15	Human	PAP	32	
RSPIDTFPTDPIKES		15	Human	PAP	47	
FGQLTQLGMEQHYEL		15	Human	PAP	67	
DRTLMSAMTNLAALF		15	Human	PAP	110	
MSAMTNLAALFPPEG		15	Human	PAP	114	
MTNLAALFPPEGVSI		15	Human	PAP	117	
PEGVSIWNPILLWQP		15	Human	PAP	126	
GVSIWNPILLWQPIP		15	Human	PAP	128	
WNPILLWQPIPVHTV		15	Human	PAP	132	
NPILLWQPIPVHTVP		15	Human	PAP	133	
PILLWQPIPVHTVPL		15	Human	PAP	134	
ILLWQPIPVHTVPLS		15	Human	PAP	135	
WQPIPVHTVPLSEDQ		15	Human	PAP	138	
LSGLHGQDLFGIWSK		15	Human	PAP	194	
YDPLYCESVHNFTLP		15	Human	PAP	210	
LPSWATEDTMTKLRE		15	Human	PAP	223	
LRELSELSLLSLYGI		15	Human	PAP	235	
LSELSLLSLYGIHKQ		15	Human	PAP	238	
LSLLSLYGIHKQKEK		15	Human	PAP	241	
KSRLQGGVLVNEILN		15	Human	PAP	255	
GGVLVNEILNHMKRA		15	Human	PAP	260	
IPSYKKLIMYSAHDT		15	Human	PAP	277	
YKKLIMYSAHDTTVS		15	Human	PAP	280	
LIMYSAHDTTVSGLQ		15	Human	PAP	283	
DTTVSGLQMALDVYN		15	Human	PAP	290	
ALDVYNGLLPPYASC		15	Human	PAP	299	
LDVYNGLLPPYASCH		15	Human	PAP	300	

HLA-DR SUPERTYPE					
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
YNGLLPPYASCHLTE		15	Human	PAP	303	
FAELVGPVIPQDWST		15	Human	PAP	356	
TVPLSEDQLLYLPFR		15	Human	PAP	145	
LTELYFEKGEYFVEM		15	Human	PAP	315	
GPVIPQDWSTECMTT		15	Human	PAP	361	
QAHSLERVCHCLGKW LGHPDK		21	Human	PLP	130	
WTTCQSIAFPSKTSASI GSL		20	Human	PLP	181	
QKGRGYRGQHQAHS LERVCH		20	Human	PLP	121	
AATYNFAVLKLMGR GTKF		18	Human	PLP	260	
VATGLCFFGVALFCG CGHEA		20	Human	PLP	21	
FLYGALLLAEGFYTT GAVRQ		20	Human	PLP	81	
SAVPVYIYFNTWTTC QSIAF		20	Human	PLP	171	
TLSVTWIGAAPLILS		15	Human	PSA	5	
SVTWIGAAPLILSRI		15	Human	PSA	7	
VTWIGAAPLILSRIV		15	Human	PSA	8	
SQPWQVLVASRGRAV		15	Human	PSA	31	
GRAVCGGVLVHPQW V		15	Human	PSA	42	
GVLVHPQWVLTAAH C		15	Human	PSA	48	
HPQWVLTAAHCIRNK		15	Human	PSA	52	
QWVLTAAHCIRNKSV		15	Human	PSA	54	
AHCIRNKSVILLGRH		15	Human	PSA	60	
SVILLGRHSLFHPED		15	Human	PSA	67	
VILLGRHSLFHPEDT		15	Human	PSA	68	
GQVFQVSHSFPHPLY		15	Human	PSA	83	
VFQVSHSFPHPLYDM		15	Human	PSA	85	
PHPLYDMSLLKNRFL		15	Human	PSA	93	
SHDLMLLRLSEPAEL		15	Human	PSA	114	
HDLMLLRLSEPAELT		15	Human	PSA	115	
TDAVKVMDLPTQEPA		15	Human	PSA	129	
LHVISNDVCAQVHPQ		15	Human	PSA	172	
CAQVHPQKVTKFMLC		15	Human	PSA	180	
GGPLVCNGVLQGITS		15	Human	PSA	210	
GPLVCNGVLQGITSW		15	Human	PSA	211	
NGVLQGITSWGSEPC		15	Human	PSA	216	
RPSLYTKVVHYRKWI		15	Human	PSA	235	
HSLFHPEDTGQVFQV		15	Human	PSA	74	
PRWLCAGALVLAGGF		15	Human	PSM	18	
LGFLFGWFIKSSNEA		15	Human	PSM	35	
LDELKAENIKKFLYN		15	Human	PSM	62	
IKKFLYNFTQIPHLA		15	Human	PSM	70	
KFLYNFTQIPHLAGT		15	Human	PSM	72	
WKEFGLDSVELAHYD		15	Human	PSM	100	

HLA-DR SUPERTYPE					
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
LAHYDVLLSYPNKTH		15	Human	PSM	110	
GNEIFNTSLFEPPPP		15	Human	PSM	135	
GKVFRGNKVKNAQL A		15	Human	PSM	206	
GNKVKNAQLAGAKG V		15	Human	PSM	211	
EYAYRRGIAEAVGLP		15	Human	PSM	276	
AEAVGLPSIPVHPIG		15	Human	PSM	284	
AVGLPSIPVHPIGYY		15	Human	PSM	286	
IGYYDAQKLLEKMGG		15	Human	PSM	297	
TGNFSTQKVKMHIHS		15	Human	PSM	334	
TRIYNVIGTLRGAVE		15	Human	PSM	353	
ERGVAYINADSSIEG		15	Human	PSM	444	
GVAYINADSSIEGNY		15	Human	PSM	446	
DSSIEGNYTLRVDCT		15	Human	PSM	453	
NYTLRVDCTPLMYSL		15	Human	PSM	459	
CTPLMYSLVHNLTKE		15	Human	PSM	466	
DFEVFFQRLGIASGR		15	Human	PSM	520	
EVFFQRLGIASGRAR		15	Human	PSM	522	
TNKFSGYPLYHSVYE		15	Human	PSM	543	
YDPMFKYHLTVAQVR		15	Human	PSM	566	
DPMFKYHLTVAQVRG		15	Human	PSM	567	
MFKYHLTVAQVRGG M		15	Human	PSM	569	
KYHLTVAQVRGGMV F		15	Human	PSM	571	
VAQVRGGMVFELANS		15	Human	PSM	576	
RGGMVFELANSIVLP		15	Human	PSM	580	
GMVFELANSIVLPFD		15	Human	PSM	582	
VFELANSIVLPFDCR		15	Human	PSM	584	
ADKIYSISMKHPQEM		15	Human	PSM	608	
IYSISMKHPQEMKTY		15	Human	PSM	611	
PQEMKTYSVSFDSLF		15	Human	PSM	619	
TYSVSFDSLFSAVKN		15	Human	PSM	624	
VLRMMNDQLMFLER A		15	Human	PSM	660	
LRMMNDQLMFLERA F		15	Human	PSM	661	
RHVIYAPSSHNKYAG		15	Human	PSM	688	
RQIYVAAFTVQAAAE		15	Human	PSM	730	
QIYVAAFTVQAAAET		15	Human	PSM	731	
VAAFTVQAAAETLSE		15	Human	PSM	734	
YISIINEDGNEIFNT		15	Human	PSM	127	
ISIINEDGNEIFNTS		15	Human	PSM	128	
EDFFKLERDMKINCS		15	Human	PSM	183	
FFKLERDMKINCSGK		15	Human	PSM	185	
GVILYSDPADYFAPG		15	Human	PSM	224	
GAAVVHEIVRSFGTL		15	Human	PSM	391	
NSRLLQERGVAYINA		15	Human	PSM	438	

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
VAYINADSSIEGNYT		15	Human	PSM	447	
DQLMFLERAFIDPLG		15	Human	PSM	666	
KSNFLNCYVSGFHPSD		16	Human B2-µglobulin		19	
AC-NPDAENWNSQFEILE DAA		18	IEd	MHC derived	Unknown	
EYLILSARDVLAVVS		15	M. leprae		85	
YKTIAYDEEARR		12	MT		3	
GEALSTLVVNKIRGT		15	Mycobacteria	HSP60	254	
PYILLVSSKVSTVKD		15	Mycobacteria	HSP60	216	
EAVLEDPYILLVSSK		15	Mycobacteria	HSP60	210	
IAGLFLTTEAVVADK		15	Mycobacteria	HSP60	507	
ALSTLVVNKIRGTFK		15	Mycobacteria	HSP60	256	
MKHILYISFYFILVN		15	Pf	LSA1	1	
KSLLSTNLPYGRTNL			Pf	SSP2	116	
HFFLFLLYILFLVKM		15	Pf		13	
LFLLYILFLVKMNAL		15	Pf		16	
ILFLVKMNALRRLPV		15	Pf		21	
MNALRRLPVICSFLV		15	Pf		27	
SAFLESQSMNKIGDD		15	Pf		79	
LKELIKVGLPSFENL		15	Pf		132	
FENLVAENVKPPKVD		15	Pf		143	
PATYGIIVPVLTSLF		15	Pf		158	
YGIIVPVLTSLFNKV		15	Pf		161	
LLKIWKNYMKIMNHL		15	Pf		28	
MTLYQIQVMKRNQK Q		15	Pf		43	
QKQVQMMIMIKFMG V		15	Pf		57	
MIMIKFMGVIYIMII		15	Pf		63	
GVIYIMIISKKMMRK		15	Pf		70	
LYYLFNQHIKKELYH		15	Pf		285	
HFNMLKNKMQSSFFM		15	Pf		299	
LDIYQKLYIKQEEQK		15	Pf		353	
QKKYIYNLIMNTQNK		15	Pf		366	
YEALIKLLPFSKRIR		15	Pf		381	
ENEYATGAVRPFQAA		15	Pf		2	
NYELSKKAVIFTPIY		15	Pf		27	
QKILIKIPVTKNIIT		15	Pf		108	
KCLVISQVSNSDSYK		15	Pf		156	
SKIMKLPKLPISNGK		15	Pf		202	
FIHFFTWGTMFVPKY		15	Pf		220	
LCNFKKNIIALLIIP		15	Pf		242	
KKNIIALLIIPPKIH		15	Pf		246	
ALLIIPPKIHISIEL		15	Pf		251	
SMEYKKDFLITARKP		15	Pf		274	
KSKFNILSSPLFNNF		15	Pf		7	

HLA-DR SUPERTYPE					
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
FKKLKNHVLFLQMMN		15	Pf		173	
KNHVLFLQMMNVNLQ		15	Pf		177	
VLFLQMMNVNLQKQL		15	Pf		180	
NVNLQKQLLTNHLIN		15	Pf		187	
QKQLLTNHLINTPKI		15	Pf		191	
NHLINTPKIMPHHII		15	Pf		197	
YILLKKILSSRFNQM		15	Pf		239	
FNQMIFVSSIFISFY		15	Pf		250	
KVSCKGSGYTFTAYQMH		17	Rheumatiod vector	Variable region		
IAKVPPGPNITAEYGDKWLD		20	Rye grass	Lolp1	1	
TAEYGDKWLDAKSTWYGKPT		20	Rye grass	Lolp1	11	
AKSTWYGKPTGAGPKDNGGA		20	Rye grass	Lolp1	21	
GAGPKDNGGACGYKDVDKAP		20	Rye grass	Lolp1	31	
FNGMTGCGNTPIFKDGRGCG		20	Rye grass	Lolp1	51	
PIFKDGRGCGSCFEIKCTKP		20	Rye grass	Lolp1	61	
SCFEIKCTKPESCSGEAVTV		20	Rye grass	Lolp1		
AFGSMAKKGEEQNVRSAGEL		20	Rye grass	Lolp1	111	
TPDKLTGPFTVRYTTEGGTK		20	Rye grass	Lolp1	201	
VRYTTEGGTKSEVEDVIPEG		20	Rye grass	Lolp1	211	
TCVLGKLSQELHKLQ		15	Salmon	Calcitonin	6	
KLSQELHKLQTYPRT		15	Salmon	Calcitonin	11	
LHKLQTYPRTNTGSG		15	Salmon	Calcitonin	16	
KLQTYPRTNTGSGTP		15	Salmon	Calcitonin	18	
CCVLGKLSQELHKLQ		15	Salmon	Calcitonin	7	A
CSNLSTCVLGKLSQE		15	Salmon	Calcitonin	1	A
TSNLSTTVLGKLSQE		15	Salmon	Calcitonin	1	A
TTVLGKLSQELHKLQ		15	Salmon	Calcitonin	6	A
DIAAKYKELGY		11	Sperm whale	Myoglobin	141	
ALVRQGLAKVA		11	Staph.	Nase	102	
PATLIKAIDGDTVKLMYKGQ		20	Staph.	Nase	11	
TPETKHPKKGVEKYGPEASA		20	Staph.	Nase	41	
VEKYGPEASAFTKKMVENAK		20	Staph.	Nase	51	
FTKKMVENAKKIEVEFDKGQ		20	Staph.	Nase	61	
YIYADGKMVNEALVRQGLAK		20	Staph.	Nase	91	
HEQHLRKSEAQAKKEKLNIW		20	Staph.	Nase	121	
QAKKEKLNIWSEDNADSGQ		19	Staph.	Nase	131	

HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
YFNNFTVSFWLRVPK		15	TetTox		947	
FSYFPSI		7	TetTox		593	A
YSFFPSI		7	TetTox		593	A
YSYFPSIR		8	TetTox		593	A
DPNANPNVDPNANPN VNANPNANPNANP(X 4)		117	Unknown	(MAP)=(T1B)4		
QKWAAVVVPS		10	Unknown	ClassI A2	242	
TWQLNGEELIQDMEL VETRPAG		22	Unknown	ClassI Kb 216-237	216	
PEFLEQRRAAVDTYC		15	Unknown	IEBs2		
STORKUSP33			Unknown	RAGE		
DYSYLQDSDPDSFQD		15	Unknown	Tyrosinase	448	
DFSYLQDSDPDSFQD		15	Unknown	Tyrosinase	448	SAAS
QNILFSNAPLGPQFP		15	Unknown	Tyrosinase	56	SAAS
QNILLSNAPLVPQFP		15	Unknown	Tyrosinase	56	SAAS
DYSYLQDSDPDSFQD		15	Unknown	Tyrosinase	448	
KYVKQNTLKLAT		11	unknown			
P(X)KQNTLKLAT		13	unknown			A
EEDIEIIPIQEEEY		14		CD20	249	A
HQAISPRTLNSPAIF		15				
YTDVFSLDPTFTIETT		16				
YAGIRRDGLLLRLVD		15				A
LFFYRKSVWSKLQSI		15				
RPIVNMDYVVGARTF RREKR		20				
RPGLLGASVLGLDDI		15				
LYFVKVDVTGAYDTI		15				
FAGIRRDGLLLRLVD		15				
AKTFLRTLVRGVPEY		15				
YGAVVNLRKTVVNFP		15				
GTAFVQMPAHGLFPW		15				
WAGLLLDTRTLEVQS		15				
RTSIRASLTFNRGFK		15				
RVIKNSIRLTL		11				
PVIKNSIKLRL		11				
ATSTKKLHKEPATLIK AIDG		21				

TABLE 26

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
AC-NPTKHKWEAAHVAEQLAA				>900000	500000		25000	
DDYVKQYTKQYTKQNTLKK	50000		160	500000		12500		
AAAKAAAAAAAYAA	833	>900000	229	500000		12500		
AC-AAAKAAAAAAYAA	625		348					
(20)AYA(20)A(20)A(20)K(20)A(20)	50000		250	500000		8333		
AC-AAAKATAAAAYAA	50000		381					
AC-AAAKAAAAAAFAA	50000		421					
AC-AAAKATAAAA(10)AA	5000		444	500000				
AC-AAAKATAAAA(23)AA	1250		286	25000				
AAKAAAAAAA(10)AA	2500		>888.89					
AAYAAAATAKAAA	3.9		0.54	2778				
AALAAAAAAKAAA	1.9		12	152		1316		
AAEAAAATAKAAA	2500		667	500000				
AAYJJAAAAKAAA	50000		533	500000				
AAYAAAAJJKAAA	1250		308	500000				
AFLRAAAAAAFAA	50000		400	500000				
AFLRQAAAAAFAAY	2500		1000	25000				
AAFAAAKTAAAFA	1.3	1063	0.19	6.2		67		
YAAFAAAKTAAAFA	0.74		0.13	5.0		34		
AALKATAAAAAAA	50000		800	500000				
YAR(15)ASQTTLKAKT	1.5		0.46	5.2		1196		
YARF(33)QTTLKAKT	50000		889	16667				
PKYFKQRILKFAT	1667		400	1042				
PKYFKQGFLKGAT	50000		800	500000				
PKYGKQIDLKGAT	50000		444	500000				
AAFFFFFGGGGGA	50000		800	500000				
AADFFFFFFFFDA	1250		286	500000				
AAKGIKIGFGIFA	50000		471	500000				
AAFIFIGGGKIKA	50000		195	500000				
AAKIFIGFFIDGA	1250		200	25000				
AAFIGFGKIKFIA	50000		242	500000				
AAKIGFGIKIGFA	50000		889	500000				
AAFKIGKFGIFFA	50000		615	500000				
AADDDDDDDDDDA	50000		667	500000				
(43)AAIGFFFFKKGIA	50000		258	500000				

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
(43)AAFFGIFKIGKF A	50000		381	500000				
(43)AADFGIFIDFIIA	50000		235	500000				
(43)AAIGGIFIFKKD A	50000		800	500000				
(43)AAFIGFGKIKFI A	50000		1000	500000				
(43)AAKIGFGIKIGF A	50000		1000	500000				
(43)AAFKIGKFGIFF A	50000		276	500000				
AAAKAAAAAAAA F	>1666.67		>347.83	12500				
AAAKAAAAAAAF A	50000		727	500000				
AAAKAAAAAAFA A	50000		235	25000				
AAAKAAAAFAAA A	50000		533	500000				
FAAAAAAAAAAA A	1667		200	8333				
AAAAAAAAAAAA N	50000		500	500000				
AAAAAAAAAAAN A	50000		1000	500000				
AAANAAAAAAAA A	50000		615	500000				
AAAAAAAAAAAA S	50000		533	500000				
AAAAASAAAAAA A	50000		235	500000				
ASAAAAAAAAAA A	50000		364	500000				
AFAAAKTAA	50000		571	500000				
YARFLALTTLRAR A	0.98		0.28	3.4				
YAR(15A)SQTTLKA KT	2.4		0.78	5.2		1786		
YAR(15A)RQTTLKA AA	1.6		0.35	3.8		8333		
(15A)RQTTLKAAA	4.2		0.31	4.3		250000		
(16A)RQTTLKAAA	455		1.3	37		250000		
(46)AAKTAAAFA	5000		571	1852				
(39)AAAATKAAA	3333		727	500000				
(52)AAAATKAAAA	2000		242	2632				
(55)AAAATKAAAA	2500		667	5556				
A(14)AAAKTAAA	39		0.45	54		96		
AA(14)A(35)ATKAA AA	50000		>500	500000				
AA(14)AA(36)TKAA AA	50000		667	25000				
AFAAAKTAA(72)	5000		533	500000				
(49)AAAKT(64)AAA	50000		667	500000				
(49)AAAKTA(64)AA	50000		533	500000				
HQAISPRTLNGPGP GSPAIF	1555	728464	12089	2056	3107	5081		
YAAFAAAKTAAAF A	1.9		0.82	7.0				
TEGRCLHYTVDKS KPK	1667		200	500000		>250000		
AWVAWRNRCK	50000		667	500000		>12500		
IVSDGNGMNAWV AWRNRC	1250	18371	1000	8333		>8333.33		

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
PHHTALRQAILSW GELMTLA	1250		166	1773		14434		
WMYYHGQRHSDE HHH	50000	>900000	727	500000		>250000		
YIVMSDWTGGA	50000	13416	222	500000		12500		
AHAAHAAHAAHA AHAA	263		80000	500000		>250000		
MDIDPYKEFGATV ELLSFLPSDFFP	1563		170			6609		
GMLPVCPLIPGSST TSTGP	1250	>900000	400	1220		250000		
LGFFPDHQLDPAFR ANT	1667	12027	333	2941		250000		
GYKVLVLNPSV	16	72407	27	2116	145	1516	115	8789
LMAFTAAVTS	2511	>73952.34	321	20577	627	240	>40562.91	160
TFALWRVSAEEY	>5279.83	88348	342	569	72	927	1433	517
ALWRVSAEEY	>6337.14	>76595.74	6543	6669	>35315.99	7954	4099	698
EEYVEIRQVGDFH	>1957.71	74884	>5365.53	11627	26	11323	13890	11154
VGGVYLLPRRGPR LGV	177	236639	22323	12756	2764	351		
VGGAYLLPRRGPR LGV	131	308534	26164	125056	>12230.45	703		
VGGVALLPRRGPR LGV	849	326288	48233	23669	>12230.45	61558		
VGGVYALPRRGPR LGV	134	348950	25750	30504	>12230.45	749		
VGGVYLAPRRGPR LGV	746	202660	33672	>116550.12	>12230.45	878		
VGGVYLLARRGPR LGV	60	23276	485	4396	2199	595		
VGGVYLLPARGPR LGV	12	68070	3644	3213	4579	49		
VGGVYLLRRAGPR LGV	202	39751	12252	32330	6432	433		
GAPLGGAARALAH GV	690	3145	10408	19762	>13044.97	10773		
GAALGGAARALAH GV	1081	26944	21362	60600	>13044.97	29786		
GAPLAGAARALAH GV	588	2983	39885	19692	>13044.97	8178		
GAPLGAAARALAH GV	226	17703	10255	52041	>13044.97	6490		
GAPLGGLARALAH GV	537	351525	13941	6564	>13044.97	66		
GAPLGGALRALAH GV	68	>486486.49	14977	977	1271	1418		
GAPLGGAAAALAH GV	147	82088	5472	1272	>3365.21	31907		
GAPLGGAARLLAH GV	398	22959	14984	21017	>3365.21	57549		
GAPLGGAARAAAH GV	797	377964	25279	>110132.16	>3365.21	31308		
GAPLGGAARALAA GV	541	23298	11270	16747	>3365.21	7419		
FPDWQNYTPGPGT RF	13766	>223880.6	23394	>109170.31	>10101.01	59625	592	3013
RFPLTFGWCFKLVP V	5913	406579	316	21384	121	4100	748	1848
RQDILDLWVYHTQ GY	2390	98327	1202	1624	1136	1628	5039	1665
RQEILDLWVYHTQ GF	1050	10530	5928	1414	3362	3052	2730	3679
LSHFLKEKGGLEGL I	537	>340909.09	2442	86814	2114	13676	1561	23191
LSFFLKEKGGLDGL I	172	>340909.09	1275	>109170.31	983	19957	1127	3501
LEPWNHPGSQPKT ACT	>33557.05	>328467.15	>33333.3 3	>96525.1	>8232.24	>72254.34	69223	34468

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
QVCFITKGLGISYGR	114	166744	1529	1391	295	91	41	296
QLCFLKKGLGISYGR	185	158381	4436	1613	443	3634	40	200
PPEESFRFGEEKTTPS	>2500	>900000	267	500000		>12500		
CIVYRDGNPYAVCDK	8464		147	1084	3473	>17182.13		31865
HYCYSLYGTTLEQQY	546		1127	9713	76	9858		12359
CYSLYGTTLEQQYNK	1086		1317	2836	71	>9964.13		25989
NTSLQDIEITCVYCK	>12106.54		10930	6143	4584	>17182.13		30884
VFEFAFKDLFVVYRD	6716		1059	2156	120	11583		16797
EFAFKDLFVVYRDSI	8944		2220	11721	33	3688		1882
DLFVVYRDSIPHAAC	1186		82	218	3591	5213		2374
FVVYRDSIPHAACHK	587	200	10	87	704	5085		2122
NTGLYNLLIRCLRCQ	127	13429	686	358	258	6743		4759
IRCLRCQKPLNPAEK	7240		6334	8464	1229	16787		32024
PRKLHELSSALEIPY	156	16146	5276	694	80	103		213
EIPYDELRLNCVYCK	3299		15532	11292	7321	>35612.54		>39432.18
TEVLDFAFTDLTIVY	2073	1542	185	1083	871	1432		349
VLDFAFTDLTIVYRD	354	30	313	6061	721	230		252
DFAFTDLTIVYRDDT	463	23	80	3373	40	725		1443
TIVYRDDTPHGVCTK	3798		22	1269	>9753.59	>35612.54		>39144.05
WYRYSVYGTTLEKLT	163	26561	249	3448	8.5	107		284
ETTIHNIELQCVECK	3623		1996	3327	6561	>35612.54		>39432.18
SEVYDFAFADLTVVY	31	2996	260	2180	101	1850		174
VYDFAFADLTVVYRE	173		119	5281	133	7012		155
DFAFADLTVVYREGN	3293		141	4948	60	1728		322
TVVYREGNPFGICKL	168		121	1833	>13089.91	10064		2407
GNPFGICKLCLRFLS	189		1227	2073	377	13916		45631
NYSVYGNTLEQTVKK	14059		1933	91506	822	>14602.8		47481
KKPLNEILIRCIICQ	1363		315	1070	347	7972		13328
NEILIRCIICQRPLC	7945		11739	23082	7704	16901		26483
IRCIICQRPLCPQEK	7549		5960	23092	2973	>14602.8		40269
CIVYRDCIAYAACHK	1166		928	8560	3973	>14602.8		10186
NTELYNLLIRCLRCQ	1108		1366	1293	873	>14602.8		12528
IRCLRCQKPLNPAEK	7012		6668	9890	8982	>14602.8		>32271.94
REVYKFLFTDLRIVY	8.7	23	112	738	52	54		204
RIVYRDNNPYGVCIM	524	325	20	432	2307	8307		24147
NNPYGVCIMCLRFLS	1075		1378	2522	454	12020		30895

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
EERVKKPLSEITIRC	1286		11896	9772	1470	9454		19968
IRCIICQTPLCPEEK	10847		12270	3812	1407	25186		28062
EIPLIDLRLSCVYCK	7610		1876	5012	336	10468		1961
SCVYCKKELTRAEVY	6466		2411	7510	465	8446		2010
VCLLFYSKVRKYRYY	960	276	286	987	73	258		1798
YYDYSVYGATLESIT	1008		186	9855	230	744		1403
IRCYRCQSPLTPEEK	10947		13358	83166	10327	13356		>36023.05
VYDFVFADLRIVYRD	98	2.2	475	5856	717	5962		198
DFVFADLRIVYRDGN	6699		867	7197	133	9847		1962
RIVYRDGNPFAVCKV	116	144	19	209	1812	6638		4962
GNPFAVCKVCLRLLS	134	3805	322	522	56	1034		29300
KKCLNEILIRCIICQ	9357		424	1229	365	16288		3997
NEILIRCIICQRPLC	10992		14069	9339	4621	18947		22062
RTAMFQDPQERPRKL	9372	154	28192	39014	7977	32947		>25346.4
LFVVYRDSIPHAACH	131	62	3.0	24	690	1998		2855
LTIVYRDDTPHGVCT	>15384.62	187	23	203	>8593.4	>72254.34		>25346.4
LCIVYRDCIAYAACH	996	1855	357	1293	628	40121		10660
YKFLFTDLRIVYRDN	109	8.8	292	256	91	1516		1255
YNFACTELKLVYRDD	7522	346	1976	4246	3147	2867		2084
LKLVYRDDFPYAVCR	778	237	123	9269	830	28971		18677
YDFVFADLRIVYRDG	1160	13	1914	3264	829	21352		5419
LRIVYRDGNPFAVCK	142	181	16	25	557	8985		14207
HEYMLDLQPETTDLY	1377		222	3997	2291	>18559.76		21277
TLRLCVQSTHVDIRT	1517		11996	8650	169	3257		6368
IRTLEDLLMGTLGIV	16	5211	95	43	61	895		1718
LEDLLMGTLGIVCPI	104		1136	353	1116	261		1994
DLLMGTLGIVCPICS	966		1324	984	639	963		2614
KATLQDIVLHLEPQN	1204		1987	811	1173	9094		17726
IDGVNHQHLPARRAE	1060		34272	165545	>16971.86	>18559.76		>39914.85
LRAFQQLFLNTLSFV	1.5	648	7.4	13	8.3	75		174
FQQLFLNTLSFVCPW	118	1321	134	1585	222	134		2062
QDYVLDLQPEATDLH	13441		253	45281	5585	>18559.76		>39914.85
DIRILQELLMGSFGI	88	3252	166	290	552	1591		282
IRILQELLMGSFGIV	67	31840	724	710	1208	1998		271
ELLMGSFGIVCPNCS	628		1078	8518	1853	4183		949
KEYVLDLYPEPTDLY	5949		131	89674	391	>72254.34		>49867.02
LRTIQQLLMGTVNIV	13	23182	108	208	179	513		181

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
IQQLLMGTVNIVCPT	71	93701	107	483	624	444		156
QLLMGTVNIVCPTCA	1192		2874	10062	4688	2947		2209
RETLQEIVLHLEPQN	1592		2941	6583	829	25856		19109
LRTLQQLFLSTLSFV	8.3	801	18	18	9.0	60		166
LQQLFLSTLSFVCPW	121	2045	113	754	94	272		152
KDYILDLQPETTDLH	6409		1022	30309	2771	>72254.34		>49867.02
LRTLQQMLLGTLQVV	80	>3750000	437	644	79	6909		5077
LQQMLLGTLQVVCPG	168		1496	631	1068	929		1692
QMLLGTLQVVCPGCA	957		2773	425	3074	3722		2082
VPTLQDVVLELTPQT	16056		214	4764	5409	>35360.68		>30612.24
LQDVVLELTPQTEID	1487		101	1094	417	5673		2180
QDVVLELTPQTEIDL	1269		83	1537	53	2716		1684
CKFVVQLDIQSTKED	1251		196	1642	374	4547		19282
VVQLDIQSTKEDLRV	1060		11122	8625	46	3762		13906
DLRVVQQLLMGALTV	8.4	25971	325	89	84	508		1845
LRVVQQLLMGALTVT	5.7	21650	115	28	85	82		204
VQQLLMGALTVTCPL	10	34257	239	614	116	71		180
QQLLMGALTVTCPLC	75		1142	1286	201	743		1170
QLLMGALTVTCPLCA	54	>3750000	595	870	1019	389		303
REYILDLHPEPTDLF	154		132	9957	354	7257		29316
TCCYTCGTTVRLCIN	1230	19884	719	2269	132	63		1374
VRTLQQLLMGTCTIV	36	32360	322	39	114	1820		496
LQQLLMGTCTIVCPS	197		1147	483	522	2098		1638
MLDLQPETTDLYCYE	10076	720	1913	12241	4249	>72254.34		>32230.34
VLDLYPEPTDLYCYE	11201	121	203	2193	212	>72254.34		>32230.34
LREYILDLHPEPTDL	134	891	23	9235	968	21989		16462
HIEFTPTRTDTYACRV	50000	30000	667	10000		>12500		
LWWVNNESLPVSPRL		315						
YEEYVRFDSDVGE	50000		400	500000		250000		
EEYVRFDSDVGE	50000		216	500000		250000		
APPRLICDSRVLERY	1374	6.3	9735	5794	7141	8937	11214	9348
ICDSRVLERYLLEAK	2758	236	1984	10984	11016	57605	808	>78947.37
VLERYLLEAKEAENI	933	59010	2598	12139	5019	13067	3150	6382
EHCSLNENITVPDTK	9837	27481	2294	28297	1205	32375	6191	>78947.37
NENITVPDTKVNFYA	>24154.59	4.8	>21390.37	7612	>18572.83	42846	1850	>78947.37
VPDTKVNFYAWKRME	2764	259	1742	4131	1328	38622	422	>78947.37

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
VNFYAWKRMEVGQQA	193	2871	10	291	15	40163	35	1238
WKRMEVGQQAVEVWQ	62	514	24	2591	94	46062	139	14696
VGQQAVEVWQGLALL	161	>174081.24	10294	6283	923	4230	>40511.09	>78947.37
VEVWQGLALLSEAVL	86	13293	1310	1357	79	6863	13411	8151
GLALLSEAVLRGQAL	83	816	11	21	1435	4606	2000	15148
SEAVLRGQALLVNSS	11	70855	2064	4207	17446	1087	>63636.36	>78947.37
RGQALLVNSSQPWEP	1118	93874	1697	1168	3434	319	29454	8450
LVNSSQPWEPLQLHV	2178	26138	>21505.38	13031	19689	8344	16920	>78947.37
QPWEPLQLHVDKAVS	11567	4862	1296	6135	1111	24157	>63636.36	34819
LQLHVDKAVSGLRSL	192	22	9.7	44	13571	3213	801	>78947.37
DKAVSGLRSLTTLLR	13	4331	1014	25	247	615	16375	>78947.37
GLRSLTTLLRALGAQ	8.5	2345	24	9.2	30	509	14	1136
TTLLRALGAQKEAIS	19	107164	339	199	103	4281	652	4607
ALGAQKEAISPPDAA	194	>204081.63	>21505.38	93062	13015	>71225.07	>60214.56	15337
KEAISPPDAASAAPL	15531	48560	6590	4389	28755	6661	6391	5735
PPDAASAAPLRTITA	309	14900	566	68	1555	24937	>63636.36	8674
SAAPLRTITADTFRK	1166	1262	1185	261	1456	3646	28110	2505
RTITADTFRKLFRVY	148	139	1042	928	1957	3448	792	4692
DTFRKLFRVYSNFLR	12	6946	70	104	93	10	39	307
LFRVYSNFLRGKLKL	43	6156	643	1816	1275	5.5	28	3508
SNFLRGKLKLYTGEA	143	9583	2883	2375	7182	3783	1433	8099
KLKLYTGEACRTGDR	122	18435	5964	3505	36294	8082	7683	2860
APPRLITDSRVLERY	10144	15	6680	3168	7765	629	26382	8391
ITDSRVLERYLLEAK	1571	6501	1303	1990	13339	7498	967	>78947.37
EHTSLNENITVPDTK	43921	33635	12379	2769	1245	37154	>16333.33	>78947.37
KLKLYTGEATRTGDR	178	118459	15	3230	1426	8234	2008	>78947.37
PQPFRPQQPYPQ								
PFRPQQPYPQ								
PQPFRPQQPYP								
PQPFRPQQP								
KQPFRPQQPYPQ								
PKPFRPQQPYPQ								
PQPFKPQQPYPQ								
PQPFRKQQPYPQ								
PQPFRPQKPYPQ								
PQPFRPQQPKPQ								
PQPFRPQQPYKQ								
PQPFRPQQPYPK								

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
QFLGQQQPFPPQ								
FLGQQQPFPPQ								
LGQQQPFPPQ								
QFLGQQQPFPP								
QFLGQQQPF								
IRNLALQTLPAMCNVY								
NLALQTLPAMCNVY								
LALQTLPAMCNVY								
IRNLALQTLPAM								
IRNLALQTLP								
EGDAFELTVSCQGGLPK			572	3578				
ESTGMTPEKVPVSEVMGT	>50000	>47368.42	510	>71428.57		>31250		
FPTIPLSRLFDNASL	8071	114611	228	22	7210	3175	4969	9876
RLFDNASLRAHRLHQ	89	97	77	2043	10328	1921	14985	23832
LRAHRLHQLAFDTYQ	162	15603	5076	2197	10139	123	5621	15115
QLAFDTYQEFEEAYI	>20491.8	7981	>10738.26	33446	5399	2580	>33333.33	>59523.81
QEFEEAYIPKEQKYS	>20491.8	>171755.73	>21276.6	>88339.22	395	31344	>33333.33	>59523.81
IPKEQKYSFLQNPQT	128	49978	217	3633	9.0	8305	13553	79800
SFLQNPQTSLCFSES	595	8617	6376	16880	>25832.77	48620	>33333.33	93856
TSLCFSESIPTPSNR	604	182762	48	229	852	1064	>33333.33	4395
REETQQKSNLELLRI	8921	91054	9341	1324	1433	51179	22467	9680
SNLELLRISLLLIQS	72	43487	621	189	379	642	>33333.33	3422
ISLLLIQSWLEPVQF	184	27922	885	177	0.86	83	>33333.33	6247
SWLEPVQFLRSVFAN	11	167103	1128	152	883	589	3416	3998
FLRSVFANSLVYGAS	4.3	15221	6.7	43	59	16	13436	15127
NSLVYGASDSNVYDL	7313	81158	190	1585	1055	201	>33333.33	3896
SDSNVYDLLKDLEEG	24369	54982	11032	>25680.53	95	182355	>33333.33	>59523.81
GIQTLMGRLEDGSPR	98	>55900.62	11914	2458	3745	18952	>33333.33	37821
RLEDGSPRTGQIFKQ	15693	76675	7906	1729	22125	35120	>33333.33	>59523.81
RTGQIFKQTYSKFDT	1555	20341	1680	1831	40	46	16432	8515
QTYSKFDTNSHNDDA	17352	>55900.62	97	11218	78	54569	7726	31341
TNSHNDDALLKNYGL	16457	26397	20308	>25680.53	16329	245523	>33333.33	>59523.81
ALLKNYGLLYCFRKD	137	9819	446	1286	551	11915	>33333.33	676
DMDKVETFLRIVQCR	1277	4813	867	1135	622	10484	1673	16127
FLRIVQCRSVEGSCGF	106	33536	185	164	191	7199	7262	5311
FPTIPLSRLFDNAML	6923	46707	9458	175	923	5529	1051	14964
RLFDNAMLRAHRLHQ	2.3	27	6289	1520	4247	3297	212	>59523.81
QLAFDTYQEFEQNPQ	>17985.61	7851	28586	47399	4843	21064	>33333.33	>59523.81

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SFLQNPQTSLCCFRK	106	1829	671	1816	1230	7026	7069	3082
SNLELLRICLLLIQS	731	61913	1526	2303	1112	1222	19782	3970
ICLLLIQSWLEPVQF	8511	50874	11303	5708	71	643	>33333.33	>59523.81
NSLVYGASDSNIYDL	13068	>51428.57	240	3683	1229	297	>33333.33	>59523.81
SDSNIYDLLKDLEEG	>17985.61	124500	17458	25922	137	>85034.01	>33333.33	50134
DKVETFLRIVQCCGF	953	18325	1158	259	397	697	581	4080
SFLQNPQTSLTFSES	1191	2395	7780	15527	9558	6197	>33333.33	17714
TSLTFSESIPTPSNR	182	17425	18	98	686	682	17602	2461
ALLKNYGLLYTFRKD	19	5982	160	266	303	5923	3616	2628
LLYTFRKDMDKVETF	>17985.61	23871	10623	17771	1133	53362	10448	>59523.81
DMDKVETFLRIVQTR	1111	11194	2030	133	454	436	183	51511
FLRIVQTRSVEGSTGF	6.4	3944	11	16	99	9.8	445	778
HLDMLRHLYQGCQVV	304	37552	9417	2741	3593	27027	5384	12508
RLRIVRGTQLFEDNYAL	4.8	11287	8389	2929	1024	12	6325	1834
GVGSPYVSRLLGICL	19	167949	1570	49	4156	190	1317	2614
TLERPKTLSPGKNGV	10103	134367	>22471.91	103285	>28592.93	25988	>75384.62	>300000
KIFGSLAFLPESFDGDPA	597	74162	1195	1897	37	377	>75384.62	15796
ELVSEFSRMARDPQ	201	1026	120	4882	15120	21259	4082	91575
GEALSTLVLNRLKVG	719	11783	3045	305	14802	3191	192	20167
AYVLLSEKKISSIQS	78	136	943	359	9471	3848	27	3338
VASLLTTAEVVVTEI	604	136308	7431	810	6517	369	>118357.49	1955
KCEFQDAYVILLSEKK	14	5791	73	943	351	336	489	185
ALSTLVLNRLKVGLQ	49	153	517	31	2167	647	4.0	2166
MSYNLLGFLQRSSNC	115	156715	366	1584	788	1060	3421	3646
LGFLQRSSNCQCQKL	437	112406	120	401	827	767	218	3729
RSSNCQCQKLLWQLN	9665	>191897.65	1046	2987	12652	9689	4530	74405
QCQKLLWQLNGRLEY	181	133472	360	460	1004	3702	2519	4669
LWQLNGRLEYCLKDR	1108	2356	816	8882	1024	10586	>16333.33	5206
GRLEYCLKDRRNFDI	9854	853	918	4155	3238	12108	1318	25159
RNFDIPEEIKQLQQF	6969	26262	18107	5375	>114457.83	47893	>144117.65	>77319.59
PEEIKQLQQFQKEDA	1026	40154	1618	618	7875	49505	11908	>77319.59
QLQQFQKEDAAVTIY	85	17383	231	27473	1121	500	4862	55351
QKEDAAVTIYEMLQN	8376	>156521.74	9437	75877	785	45455	>144117.65	5989
AVTIYEMLQNIFAIF	17	23730	101	808	163	267	6873	4540
EMLQNIFAIFRQDSS	395	9544	685	689	456	3313	10429	9738
IFAIFRQDSSSTGWN	132	402	9.6	71	118	1186	4725	970
RQDSSSTGWNETIVE	>102040.82	38681	4637	184507	40847	36320	15135	9075

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STGWNETIVENLLAN	21407	>156521.74	1755	10422	7060	3960	>144117.65	>77319.59
ETIVENLLANVYHQR	659	40053	789	802	326	21681	>144117.65	8151
NLLANVYHQRNHLKT	152	40328	1039	1440	1492	8000	453	4160
VYHQRNHLKTVLEEK	617	3135	7757	76003	153	6180	2101	>77319.59
LEKEDFTRGKRMSSL	21965	50733	>20887.73	93968	5694	946	804	>77319.59
FTRGKRMSSLHLKRY	13	3302	1013	970	484	136	553	10925
RMSSLHLKRYYGRIL	275	2181	993	4793	34	283	277	14964
HLKRYYGRILHYLKA	26	3709	135	666	86	214	237	2896
YGRILHYLKAKEDSH	30	42429	2343	917	23	900	704	7577
HYLKAKEDSHCAWTI	1128	34758	2064	12153	3701	581	34851	>77319.59
KEDSHCAWTIVRVEI	4835	>46656.3	353	1090	74	30	40000	2937
CAWTIVRVEILRNFY	66	3561	158	640	135	746	43672	757
VRVEILRNFYVINRL	1.8	429	140	47	18	14	3585	485
RNFYVINRLTGYLRN	1.7	2199	219	4618	182	527	167	7600
MSYNLLGFLQRSSNT	25	107838	1152	813	433	8867	900	8972
LGFLQRSSNTQTQKL	142	26455	18	211	1068	420	939	1345
RSSNTQTQKLLWQLN	10515	44338	2139	15497	12590	27678	1283	>77319.59
QTQKLLWQLNGRLEY	32	3555	55	35283	86	3099	2042	2083
LWQLNGRLEYTLKDR	698	511	757	16171	94	20198	43286	16619
GRLEYTLKDRRNFDI	7252	30	3228	97035	1379	4961	4917	>77319.59
HYLKAKEDSHTAWTI	232	70237	553	10677	15067	801	8526	10140
KEDSHTAWTIVRVEI	1909	44754	746	2178	302	35	>79032.26	6079
TAWTIVRVEILRNFY	7.8	2997	44	84	115	29	57243	404
LGFLQRSSNCQSQKL	192	4888	8.1	93	228	305	405	13167
RSSNCQSQKLLWQLN	2050	57946	595	16721	4010	8922	6943	4062
QSQKLLWQLNGRLEY	127	33374	84	741	55	1166	991	5920
GIVEQCCTSICSLYQ	11123	777105	10911	2995	17793	>79872.2	>10047.16	13855
TSICSLYQLENYCN	11391	>154109.59	20462	3791	12457	>85616.44	>54444.44	>63025.21
GILEQCCTSICSLYQ	11025	>187500	14862	5106	15983	54113	>54444.44	16714
GIVEQTTTSITSLYQ	6354	107486	121	115	818	788	>54444.44	13304
EQTTTSITSLYQLEN	18953	>143769.97	170	258	272	2230	>54444.44	17381
TSICSLYQLENYCG	1125	202253	8841	1986	1089	247525	>54444.44	>83333.33
TSITSLYQLENYTN	1253	81293	1468	138	851	6055	26791	9947
TSITSLYQLENYTG	1132	96727	1628	129	115	8371	14562	46268
GIVEQCCCGSHLVEA	10043	>74750.83	19904	2892	6626	41276	>54444.44	>63025.21
SLYQLENYCCGERGF	3568	54469	7313	1527	2356	12308	>54444.44	>83333.33
CCTSICSLYQLENYCC	11655	71239	8383	1604	629	35604	>54444.44	29845

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
GSHLVEALYLVCCN	194	>59681.7	2280	11512	2509	302	>54444.44	37166
CCGSHLVEALYLVCC	880	>55693.07	10081	20487	5230	1822	>54444.44	>63025.21
FVNQHLCGSHLVEAL	583	>187500	19209	39746	>20663.4	6791	>54444.44	>63025.21
QHLCGSHLVEALYLV	170	48557	12954	4303	9825	86	>54444.44	7422
GSHLVEALYLVCGER	525	>187500	8292	1603	4609	560	>54444.44	5386
VEALYLVCGERGFFY	76	17558	209	124	1044	3869	24623	2233
YLVCGERGFFYTPKT	11063	37210	1439	22980	730	64644	>54444.44	1520
FVNQHLCGSDLVEAL	117	>74750.83	19154	36693	14913	38662	>54444.44	>63025.21
FVNQHLTGSHLVEAL	9.2	67240	858	14916	1065	15	>54444.44	41482
QHLTGSHLVEALYLV	9.3	50338	>16096.58	3952	7423	38	>54444.44	42312
GSHLVEALYLVTGER	645	>176470.59	15781	1693	14443	553	>54444.44	>63025.21
VEALYLVCGERGSFY	88	9972	833	194	6108	6485	>54444.44	6311
VEALYLVCGERGFLY	14	11587	167	31	1027	5351	10565	3063
VEALYLVTGERGFFY	9.9	2011	60	23	2342	195	1224	683
YLVCGERGFLYTPKT	155	2033	>20460.36	>38550.5	>30134.81	12842	>54444.44	124
YLVCGERGFFYTDKT	17260	11790	>20460.36	>38550.5	>30134.81	92272	>54444.44	317
YLVCGERGFFYTKPT	3207	42139	>20460.36	>38550.5	>30134.81	969	>54444.44	1673
YLVTGERGFFYTPKT	779	517	>20460.36	>38550.5	30457	7737	29236	6295
YLVTGERGFFYTDKT	3259	7326	>20460.36	>38550.5	>30134.81	5328	>25789.47	2909
YLVTGERGFFYTKPT	1152	4801	>20460.36	>38550.5	>30134.81	78	4304	195313
VCGERGFFYTPKTRR	9622	1989	>20460.36	>38550.5	>15103.34	5494	419	14379
VTGERGFFYTPKTRR	18906	3018	7226	147000	13417	27824	9407	>300000
MWDLVLSIALSVGCT	205		1846			3032	23046	1727
DLVLSIALSVGCTGA	1197		13038			4029	>245000	2200
HPQWVLTAAHCLKKN	22	1103	875			563	1693	822
QWVLTAAHCLKKNSQ	895		>40000			3402	98000	4813
GQRVPVSHSFPHPLY	1563		>40000			629	>245000	102
RVPVSHSFPHPLYNM	67		>16000			101	100021	97
PHPLYNMSLLKHQSL	19079		819			20691	3315	1592
HPLYNMSLLKHQSLR	232	13007	499			1282	382	199
NMSLLKHQSLRPDED	3131		>40000			20620	26496	96825
SHDLMLLRLSEPAKI	56	2396	2244			106	1327	112
HDLMLLRLSEPAKIT	16	1406	3063			109	544	43
PEEFLRPRSLQCVSL	2001		>26666.67			5156	2207	5839
PRSLQCVSLHLLSND	1111		16000			2217	6107	28307

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
NGVLQGITSWGPEPC	1093		8433			2285	52234	50111
KPAVYTKVVHYRKWI	5000		1433			2401	53	3677
LHLLSNDMCARAYSE	2104	938	4277			27685	50230	59904
VGNWQYFFPVIFSKA	37		4.1			100		
ESEFQAALSRKVAKL			579	29617				
IGHLYIFATCLGLSYDGL			>816.33	12199				
VGNWQYFFPVIFSKASDSLQLVFGIELMEVD			654	3846				
PAYEKLSAEQSPPPY			479	>250000				
RNGYRALMDKSLHVGTQCALTRR			512	5779				
FFKNIVTFFKNIVT	50000		>666.67	500000		>12500		
YKSAHKGFKGVDAQGTLSKI	70	>900000	889	25000		108		
VDAQGTLSKIFKLGGRDSRS	25	1383	1600	314		1171		
AC-ASQKRPSQRHGSKYLATAST	50000	>900000	889	25000		2362		
ENPVVHFFKNIVTPR								
ENPVVAFFKNIVTPR								
ENPVVHAFKNIVTPR								
ENPVVHFFANIVTPR								
ENPVVHFFKNIVTPA								
NPVVHFFKNIVT								
HFFKNIVTPRTPPY								
NPVVHFFKNIVTPR								
LPVPGVLLKEFTVSGNILTI	57	15058	14	12	12	57		
WITQCFLPVFLAQPPSGQRR	679	25534	88	2804	216	74162		
DHRQLQLSISSCLQQLSLLM	1356	42666	1322	210	725	736		
YLAMPFATPMEAELARRSLA	46	46591	266	814	405	526		
AAPLLLARAASLSLG	6.8	35410	139			160	30	64
APLLLARAASLSLGF	8.4	56250	202			59	76	124
PLLLARAASLSLGFL	10	>81818.18	521			162	37	58
SLSLGFLFLLFFWLD	11417		4711			22727	>122500	24620
LLFFWLDRSVLAKEL	2.9	6.3	2.6			135	163	518
DRSVLAKELKFVTLV	705		569			2016	15815	4719
AKELKFVTLVFRHGD	787	30000	783			606	1953	2355
RSPIDTFPTDPIKES	>50000		13095			>62500	>245000	6124
FGQLTQLGMEQHYEL	2259		3210			>62500	109567	>187500
DRTLMSAMTNLAALF	97	64286	13			383	2362	222
MSAMTNLAALFPP	1757		700			36084	73870	>187500

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
EG								
MTNLAALFPPEGVSI	24		>40000			>125000	39231	22822
PEGVSIWNPILLWQP	111		1778			15030	28577	103096
GVSIWNPILLWQPIP	44	56250	10328			4992	11008	3985
WNPILLWQPIPVHTV	208	>81818.18	695			521	115494	607
NPILLWQPIPVHTVP	31	>81818.18	206			41	12999	575
PILLWQPIPVHTVPL	44	>81818.18	258			46	21244	168
ILLWQPIPVHTVPLS	45	>81818.18	170			19	13091	131
WQPIPVHTVPLSEDQ	6386		>26666.67			159	>81666.67	17518
LSGLHGQDLFGIWSK	148		>26666.67			>35714.29	>81666.67	>125000
YDPLYCESVHNFTLP	1597	16625	8889			838	30867	643
LPSWATEDTMTKLRE	20274		973			>35714.29	>81666.67	>125000
LRELSELSLLSLYGI	655		371			4010	9368	1614
LSELSLLSLYGIHKQ	482	>81818.18	1549			20906	1186	1450
LSLLSLYGIHKQKEK	656	>81818.18	4444			>35714.29	1637	4959
KSRLQGGVLVNEILN	362		>26666.67			2838	>81666.67	5516
GGVLVNEILNHMKRA	2165	700	359			29463	3239	54411
IPSYKKLIMYSAHDT	9.9	9728	510			1946	60	351
YKKLIMYSAHDTTVS	17	22678	207			292	309	107
LIMYSAHDTTVSGLQ	4496		24			731	24812	813
DTTVSGLQMALDVYN	171		4424			14706	>245000	2876
ALDVYNGLLPPYASC	18		485			>83333.33	588	86603
LDVYNGLLPPYASCH	15		348			>83333.33	404	31277
YNGLLPPYASCHLTE	42		6189			>83333.33	14027	8022
FAELVGPVIPQDWST	12		4690			24056	>245000	39472
TVPLSEDQLLYLPFR	4012	332	10755			11313	42162	37369
LTELYFEKGEYFVEM	2249	592	8051			13062	18841	26949
GPVIPQDWSTECMTT		52098						
QAHSLERVCHCLGKWLGHPDK	50000		667	500000		>250000		
WTTCQSIAFPSKTSASIGSL		17308	22					
QKGRGYRGQHQAHSLERVCH		>47368.42	88					
AATYNFAVLKLMGRGTKF		>52941.18	533					
VATGLCFFGVALFCGCGHEA		>112500	351					
FLYGALLLAEGFYTTGAVRQ								
SAVPVYIYFNTWTTCQSIAF								
TLSVTWIGAAPLILS	3.1	>81818.18	7273			16	840	5.4

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
SVTWIGAAPLILSRI	4.1	>81818.18	3152			83	139	30
VTWIGAAPLILSRIV	8.1	>81818.18	8000			195	731	82
SQPWQVLVASRGRAV	66	>81818.18	7628			385	386	621
GRAVCGGVLVHPQWV	386		>26666.67			3582	>245000	8069
GVLVHPQWVLTAAHC	87	21320	67			153	1931	365
HPQWVLTAAHCIRNK	13	3632	1621			283	1305	107
QWVLTAAHCIRNKSV	50		19403			214	2598	967
AHCIRNKSVILLGRH	578	29704	69			2573	104	715
SVILLGRHSLFHPED	717	1400	12649			26088	500	5216
VILLGRHSLFHPEDT	273	8744	8208			30625	737	18520
GQVFQVSHSFPHPLY	288	45000	8.2			27	548	33
VFQVSHSFPHPLYDM	16	>75000	25			51	8751	17
PHPLYDMSLLKNRFL	1315		20787			10699	29813	12836
SHDLMLLRLSEPAEL	532	6215	4051			58	3538	64
HDLMLLRLSEPAELT	62	2867	6193			152	3914	22
TDAVKVMDLPTQEPA	>50000		>80000			>41666.67	20875	>107142.86
LHVISNDVCAQVHPQ	789	8318	790			17451	>122500	32671
CAQVHPQKVTKFMLC	10206		2566			32275	8731	34893
GGPLVCNGVLQGITS	3353		68			>35714.29	9334	16308
GPLVCNGVLQGITSW	1724		30			4893	4187	32640
NGVLQGITSWGSEPC	945	24942	560			485	5874	819
RPSLYTKVVHYRKWI	6041	53785	339			652	39	5484
HSLFHPEDTGQVFQV		65260						
PRWLCAGALVLAGGF	46		>20000			766	26531	1439
LGFLFGWFIKSSNEA	10	>75000	1338			2261	1421	1701
LDELKAENIKKFLYN	1136	1370	4842			7470	1248	12778
IKKFLYNFTQIPHLA	449	8080	43			29	512	160
KFLYNFTQIPHLAGT	340	13805	217			30	415	54
WKEFGLDSVELAHYD	1139	85	96			3511	19971	7052
LAHYDVLLSYPNKTH	79	37533	1117			3617	415	1009
GNEIFNTSLFEPPPP	20412		>20000			>35714.29	>163333.33	10415
GKVFRGNKVKNAQLA	612		1087			2350	4121	31277
GNKVKNAQLAGAKGV	677		13333			>83333.33	28904	7882
EYAYRRGIAEAVGLP	5.1		213			70	596	67
AEAVGLPSIPVHPIG	5.4		9923			2015	>490000	23102
AVGLPSIPVHPIGYY	3.6		4193			1080	4432	15377

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
IGYYDAQKLLEKMGG	1923		12649			>83333.33	8236	47246
TGNFSTQKVKMHIHS	11180		833			9407	10282	1450
TRIYNVIGTLRGAVE	14	33333	6.3			4806	70	2900
ERGVAYINADSSIEG	2440		6761			34021	>163333.33	25516
GVAYINADSSIEGNY	1054		146			6244	23360	3048
DSSIEGNYTLRVDCT	16667		3360			14458	>163333.33	>187500
NYTLRVDCTPLMYSL	6804	45	9.9			24597	6323	48412
CTPLMYSLVHNLTKE	93	19437	245			140	223	249
DFEVFFQRLGIASGR	143		221			21926	122	2005
EVFFQRLGIASGRAR	28	>75000	22			5311	6.3	2976
TNKFSGYPLYHSVYE	3402		5521			30853	614	741
YDPMFKYHLTVAQVR	9.0	>75000	19			158	172	179
DPMFKYHLTVAQVRG	5.7	>75000	9.1			168	43	258
MFKYHLTVAQVRGGM	16	29032	18			72	70	266
KYHLTVAQVRGGMVF	137	33658	806			228	1519	5860
VAQVRGGMVFELANS	228		662			4449	>98000	499
RGGMVFELANSIVLP	10	37118	229			41	8682	33
GMVFELANSIVLPFD	15	4604	230			30	4995	81
VFELANSIVLPFDCR	19	667	999			39	36123	50
ADKIYSISMKHPQEM	22361		5310			4098	1136	3512
IYSISMKHPQEMKTY	8452		16000			11573	1357	12293
PQEMKTYSVSFDSLF	15143		3024			1192	>98000	1981
TYSVSFDSLFSAVKN	219	101	73			346	2256	526
VLRMMNDQLMFLERA	118	183	29			17334	1700	10684
LRMMNDQLMFLERAF	2704		392			17507	2492	4601
RHVIYAPSSHNKYAG	2174		481			31250	11667	481
RQIYVAAFTVQAAAE	3.7	28347	1.2			292	36	91
QIYVAAFTVQAAAET	1.6	26609	1.6			324	102	65
VAAFTVQAAAETLSE	14	>75000	58			793	1420	127
YISIINEDGNEIFNT	498	397	624			23719	>122500	83056
ISIINEDGNEIFNTS	507	559	>12965.96			>23105.36	>122500	>52337.75
EDFFKLERDMKINCS	2710	468	226			8550	1439	>52337.75
FFKLERDMKINCSGK	4419	121	483			>23105.36	8109	>52337.75
GVILYSDPADYFAPG	1566	17	7508			7848	106291	2473
GAAVVHEIVRSFGTL		12409						
NSRLLQERGVAYIN	614	318	5089			7997	3224	2616

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
A								
VAYINADSSIEGNYT	4716	531	411			9745	105832	5467
DQLMFLERAFIDPLG		>19667.83						
KSNFLNCYVSGFHPSD	2500	>900000	296	3125		8333		
AC-NPDAENWNSQFEILEDAA					500000		>25000	
EYLILSARDVLAVVS			508					
YKTIAYDEEARR	50000	143	4000	500000		250000		
GEALSTLVVNKIRGT	292	29687	1535	246	30057	2325	383	40840
PYILLVSSKVSTVKD	1.1	106	64	13	136	38	12	134
EAVLEDPYILLVSSK	34	479	233	172	681	933	1666	15032
IAGLFLTTEAVVADK	6.8	27189	13	106	67	230	3893	409
ALSTLVVNKIRGTFK	75	274	648	40	3626	396	20	18035
MKHILYISFYFILVN	5893		189		3385	1250	15558	
KSLLSTNLPYGRTNL	4226		690			50000		
HFFLFLLYILFLVKM	337		260			42443	19641	
LFLLYILFLVKMNAL	1160		283			4868	10869	
ILFLVKMNALRRLPV	0.80		5.6			56	19	
MNALRRLPVICSFLV	2.1		13			488	265	
SAFLESQSMNKIGDD	549		113			523	21493	
LKELIKVGLPSFENL	99		163			542	1493	
FENLVAENVKPPKVD	56		2372			120215	>25025.54	
PATYGIIVPVLTSLF	1.03		15			139	181	
YGIIVPVLTSLFNKV	6.0		2.0			60	793	
LLKIWKNYMKIMNHL	121		132			395	132	
MTLYQIQVMKRNQKQ	1219		117			31053	166	
QKQVQMMIMIKFMGV	121		213			3618	182	
MIMIKFMGVIYIMII	2905		312			68040	66150	
GVIYIMIISKKMMRK	10		22			476	137	
LYYLFNQHIKKELYH	27		1324			10244	1771	
HFNMLKNKMQSSFFM	12		18			3225	185	
LDIYQKLYIKQEEQK	2834		1492			>88339.22	1204	
QKKYIYNLIMNTQNK	73		24			11942	13255	
YEALIKLLPFSKRIR	55		1839			3578	180	
ENEYATGAVRPFQAA	4438		281			4970	17329	
NYELSKKAVIFTPIY	713		536			5498	141	
QKILIKIPVTKNIIT	993		303			534	2240	
KCLVISQVSNSDSY	628		16			46383	17859	

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
K								
SKIMKLPKLPISNGK	824		6485			83674	110	
FIHFFTWGTMFVPKY	745		273			489	1699	
LCNFKKNIIALLIIP	9.7		312			423	21324	
KKNIIALLIIPPKIH	13		203			495	157	
ALLIIPPKIHISIEL	648		1738			8.4	11957	
SMEYKKDFLITARKP	939		24			776	8897	
KSKFNILSSPLFNNF	0.80		16			65	152	
FKKLKNHVLFLQMMN	2.3		28			11	695	
KNHVLFLQMMNVNLQ	12		32			757	>120098.04	
VLFLQMMNVNLQKQL	6.3		30			8441	56770	
NVNLQKQLLTNHLIN	96		2460			555	11245	
QKQLLTNHLINTPKI	675		228			4412	20984	
NHLINTPKIMPHHII	1378		4798			625	1296	
YILLKKILSSRFNQM	220		183			8.3	18	
FNQMIFVSSIFISFY	483		2091			854	16504	
KVSCKGSGYTFTAYQMH	5000		381	50000		2946		
IAKVPPGPNITAEYGDKWLD	50000	>30000	>666.67	500000		>12500		
TAEYGDKWLDAKSTWYGKPT	50000	>30000	>666.67	16667		3125		
AKSTWYGKPTGAGPKDNGGA	50000	>30000	667	500000		>12500		
GAGPKDNGGACGYKDVDKAP	50000	>30000	>666.67	500000		>12500		
FNGMTGCGNTPIFKDGRGCG	50000	51962	>666.67	500000		>12500		
PIFKDGRGCGSCFEIKCTKP	50000	6784	>666.67	500000		>12500		
SCFEIKCTKPESCSGEAVTV	50000	>900000	>666.67	500000		12500		
AFGSMAKKGEEQNVRSAGEL	50000	>30000	>666.67	50000		>12500		
TPDKLTGPFTVRYTTEGGTK	50000	>900000	>666.67	500000		>12500		
VRYTTEGGTKSEVEDVIPEG	50000	>30000	>666.67	500000		>12500		
TCVLGKLSQELHKLQ	26	29529	14848	7566	9001	18653	7656	17895
KLSQELHKLQTYPRT	19	196889	19684	2076	12198	85464	28656	19129
LHKLQTYPRTNTGSG	2118	>205479.45	15182	9921	>7403.08	40226	1618	>29228.37
KLQTYPRTNTGSGTP	>10060.36	>205479.45	>26490.07	114672	>9806.45	>99206.35	>51578.95	>29228.37
CCVLGKLSQELHKLQ	34	17387	19764	31253	5299	41656	5640	21704
CSNLSTCVLGKLSQE	296	>205479.45	14339	28603	5340	31837	3516	7225
TSNLSTTVLGKLSQE	298	86798	8016	32358	9280	31275	2058	2469
TTVLGKLSQELHKLQ	133	92782	22449	36802	>9806.45	26113	16182	23824
DIAAKYKELGY		>900000	>470.59					
ALVRQGLAKVA	1250		190	500000				

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
PATLIKAIDGDTVK LMYKGQ	278	6429	296	3846		8333		
TPETKHPKKGVEK YGPEASA	>1000	>900000	>500	500000		12500		
VEKYGPEASAFTK KMVENAK	50000	>900000	1333	500000		12500		
FTKKMVENAKKIE VEFDKGQ	>1000	11619	>500	500000		8333		
YIYADGKMVNEAL VRQGLAK	65		500	4167		1563		
HEQHLRKSEAQAK KEKLNIW	50000	90000	80000	16667		6250		
QAKKEKLNIWSED NADSGQ	50000	>900000	364	3125		>250000		
YFNNFTVSFWLRV PK	50000		615	25000				
FSYFPSI	50000		889	16667				
YSFFPSI	50000		889	500000				
YSYFPSIR	50000	>900000	667	16667		7217		
DPNANPNVDPNAN PNVNANPNANPNA NP(X4)			738	>5494.51		>15625		
QKWAAVVVPS	50000		1000	50000				
TWQLNGEELIQDM ELVETRPAG	50000		889	2273				
PEFLEQRRAAVDT YC	5000		80000	500000		250000		
STORKUSP33			617	2069				
DYSYLQDSDPDSFQ D	>50000		189	>500000	>126666.67	>250000	>61250	>107142.8 6
DFSYLQDSDPDSFQ D			264	>500000	>126666.67	>250000	>61250	>107142.8 6
QNILFSNAPLGPQF P			195					
QNILLSNAPLVPQF P			538					
DYSYLQDSDPDSFQ D			316	>166666.67				
KYVKQNTLKLAT	9.9		6.2	25000				
P(X)KQNTLKLAT	1.7							
EEDIEIIPIQEEEY	>9057.97	>18549.05	>7518.8	12203	849	>6742.18		128305
HQAISPRTLNSPAIF	1961	298315	6214	1314	3450	39701	14848	286179
YTDVFSLDPTFTIET T		217						
YAGIRRDGLLLRLV D		9.6						
LFFYRKSVWSKLQ SI	19	30163	913	1383	84	84	65	
RPIVNMDYVVGAR TFRREKR	29	22	3.1	21	812	346	748	
RPGLLGASVLGLD DI	1789	35768	6522	4414	3183	506	>61250	
LYFVKVDVTGAYD TI	16	9.6	2.8	13	14	5892	413	
FAGIRRDGLLLRLV D	2381	3.6	7092	3820	>3365.21	41148	7650	
AKTFLRTLVRGVPE Y	104	54159	208	3326	105	25	9.2	
YGAVVNLRKTVVN FP	13509	150175	4194	4531	>95000	8274	113	
GTAFVQMPAHGLF PW	1.6	37275	8.1	34	18	90	99	
WAGLLLDTRTLEV QS	2016	22	49	323	1238	186	>61250	
RTSIRASLTFNRGF K	1430	256	770	177	5131	411	5475	

	HLA-DR SUPERTYPE							
Sequence	DRB1 *0101	DRB1 *0301	DRB1 *0401	DRB1 *0404	DRB1 *0405	DRB1 *0701	DRB1 *0802	DRB1 *0901
RVIKNSIRLTL	3650	584	9249	5389	80682	2239	1175	2566
PVIKNSIKLRL	1549	198	34245	14612	277735	4091	541	2851
ATSTKKLHKEPATL IKAIDG	4.6	8018	113	1020		2083		

TABLE 27

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
AC-NPTKHKWEAAHVAEQLAA		>33333.33	>10000	200000	101		1250	
DDYVKQYTKQYTKQNTLKK		>1111.11			>11111.11		35	
AAAKAAAAAAAYAA		200000			6250		2857	
AC-AAAKAAAAAAYAA(20)AYA(20)A(20)A(20)K(20)A(20)		200000					2857	
AC-AAAKATAAAAYAA								
AC-AAAKAAAAAAFAA								
AC-AAAKATAAAA(10)AA								
AC-AAAKATAAAA(23)AA								
AAKAAAAAAA(10)AA								
AAYAAAATAKAAA								
AALAAAAAAKAAA		2222					67	
AAEAAAATAKAAA								
AAYJJAAAAKAAA								
AAYAAAAJJKAAA								
AFLRAAAAAAFAA								
AFLRQAAAAAFAAY								
AAFAAAKTAAAFA		4.6			20000		25	6.4
YAAFAAAKTAAAFA		2.6			33333	30	9.5	
AALKATAAAAAAA								
YAR(15)ASQTTLKAKT		3.9					3.6	
YARF(33)QTTLKAKT								
PKYFKQRILKFAT								
PKYFKQGFLKGAT								
PKYGKQIDLKGAT								
AAFFFFFGGGGGA								
AADFFFFFFFFDA								
AAKGIKIGFGIFA								
AAFIFIGGGKIKA								
AAKIFIGFFIDGA								
AAFIGFGKIKFIA								
AAKIGFGIKIGFA								
AAFKIGKFGIFFA								
AADDDDDDDDDDA								
(43)AAIGFFFFKKGIA								
(43)AAFFGIFKIGKFA								
(43)AADFGIFIDFIIA								
(43)AAIGGIFIFKKDA								
(43)AAFIGFGKIKFIA								
(43)AAKIGFGIKIGFA								
(43)AAFKIGKFGIFFA								
AAAKAAAAAAAAF								

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
AAAKAAAAAAAFA								
AAAKAAAAAAFAA								
AAAKAAAAFAAAA								
FAAAAAAAAAAAA								
AAAAAAAAAAAAN								
AAAAAAAAAAANA								
AAANAAAAAAAAA								
AAAAAAAAAAAAS								
AAAAASAAAAAAA								
ASAAAAAAAAAAA								
AFAAAKTAA								
YARFLALTTLRARA								
YAR(15A)SQTTLKAKT		2.5					1.4	48
YAR(15A)RQTTLKAAA		1.2					0.94	62
(15A)RQTTLKAAA		1.8					9.5	3095
(16A)RQTTLKAAA		77					4000	
(46)AAKTAAAFA								
(39)AAAATKAAA								
(52)AAAATKAAAA								
(55)AAAATKAAAA								
A(14)AAAKTAAA		43					120	
AA(14)A(35)ATKAAAA								
AA(14)AA(36)TKAAAA								
AFAAAKTAA(72)								
(49)AAAKT(64)AAA								
(49)AAAKTA(64)AA								
HQAISPRTLNGPGPGSPAIF		9875	638	5570		232	32930	
YAAFAAAKTAAAFA					>4347.83			
TEGRCLHYTVDKSKPK		>1250			4082		2857	
AWVAWRNRCK		>5000			>11111.11		44	
IVSDGNGMNAWVAWRNRC		6667			>6250		>2222.22	
PHHTALRQAILSWGELMTLA		3116		5.3		48	261	
WMYYHGQRHSDEHHH		>10000			>7692.31		>5000	
YIVMSDWTGGA		>6666.67			>33333.33		>10000	
AHAAHAAHAAHAAHAA		200000					200000	
MDIDPYKEFGATVELLSFLPSDFFP			2415					
GMLPVCPLIPGSSTTSTGP		2500			>25000		200000	
LGFFPDHQLDPAFRANT		6667			1449		6667	
GYKVLVLNPSV		26	21	126		995	>11441.65	
LMAFTAAVTS		>23337.22	>2464.79	1934		11687	>12586.53	
TFALWRVSAEEY		342	>2569.75	>12709.5		>6608.93	25499	
ALWRVSAEEY		243	>6398.54	>15268.46		>7930	>35587.19	
EEYVEIRQVGDFH		4683	>1895.99	2060		2063	9754	
VGGVYLLPRRGPRLGV		88	>15350.88	4.2	60753	19239	12	

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
VGGAYLLPRRGPRLGV		507	24663	4.1	>66533.6	37640	50	
VGGVALLPRRGPRLGV		154	>15350.88	8.5	>66533.6	25688	20459	
VGGVYALPRRGPRLGV		12	>15350.88	451	>66533.6	26122	34	
VGGVYLAPRRGPRLGV		35	>15350.88	55	>66533.6	>42059.46	76	
VGGVYLLARRGPRLGV		6.5	10325	2.8	17030	4338	17	
VGGVYLLPARGPRLGV		694	201	6.5	18073	18960	40	
VGGVYLLRRAGPRLGV		67	>15350.88	6.2	91912	30707	7.9	
GAPLGGAARALAHGV		24	8739	1615	>70972.32	3959	11983	
GAALGGAARALAHGV		168	19335	4483	>70972.32	3509	25372	
GAPLAGAARALAHGV		9.5	7215	2810	>70972.32	2963	7688	
GAPLGAAARALAHGV		36	15091	3920	>70972.32	16533	4502	
GAPLGGLARALAHGV		12	76	1805	123762	3950	4256	
GAPLGGALRALAHGV		83	340	2068	>51098.62	4889	5396	
GAPLGGAAAALAHGV		43842	23810	7682	>51098.62	31	12916	
GAPLGGAARLLAHGV		80	29412	631	>51098.62	2549	26684	
GAPLGGAARAAAHGV		3633	>23489.93	>8666.67	>51098.62	41441	42463	
GAPLGGAARALAAGV		45	23179	5714	>51098.62	3865	8354	
FPDWQNYTPGPGTRF		>51282.05	>12027.49	35058		33923	>20533.88	
RFPLTFGWCFKLVPV		62289	4797	514		964	>20533.88	
RQDILDLWVYHTQGY		>51282.05	6775	723		1326	16155	
RQEILDLWVYHTQGF		11113	5384	985		1071	>20533.88	
LSHFLKEKGGLEGLI		9460	>12027.49	>39737.99		18709	>20533.88	
LSFFLKEKGGLDGLI		614	>12027.49	>39737.99		13214	15272	
LEPWNHPGSQPKTACT		>15325.67	>11041.01	2665		92	2939	
QVCFITKGLGISYGR		31	92	3555		876	3950	
QLCFLKKGLGISYGR		9.5	88	4212		282	1190	
PPEESFRFGEEKTTPS		>10000			>14285.71		>2857.14	
CIVYRDGNPYAVCDK		>14662.76	1646	650		>24786.32	>10666.67	
HYCYSLYGTTLEQQY		12397	>13725.49	4849		1292	>10666.67	
CYSLYGTTLEQQYNK		>14662.76	>13725.49	5060		189	>10666.67	
NTSLQDIEITCVYCK		>14662.76	14857	678		11710	>10666.67	
VFEFAFKDLFVVYRD		10923	7675	4871		18117	>10666.67	
EFAFKDLFVVYRDSI		9496	9996	5355		9072	5998	
DLFVVYRDSIPHAAC		1163	11172	2832		2676	10741	
FVVYRDSIPHAACHK		1194	1851	349		18144	2343	
NTGLYNLLIRCLRCQ		14	5692	67		222	598	
IRCLRCQKPLNPAEK		>14662.76	>13725.49	6928		611	>10666.67	
PRKLHELSSALEIPY		5990	51	1116		1710	>10666.67	
EIPYDELRLNCVYCK		>18001.8	858	2084		9047	>62305.3	
TEVLDFAFTDLTIVY		>18001.8	>13059.7	561		110	>62305.3	
VLDFAFTDLTIVYRD		7474	3102	645		11294	14839	
DFAFTDLTIVYRDDT		14334	5008	3651		21621	675	
TIVYRDDTPHGVCTK		>18001.8	6280	5449		>21521.34	>62305.3	
WYRYSVYGTTLEKLT		1670	805	421		1039	62	
ETTIHNIELQCVECK		>18001.8	6282	11191		112	>62305.3	

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
SEVYDFAFADLTVVY		>18001.8	>13059.7	955		1325	11802	
VYDFAFADLTVVYRE		>18001.8	>13059.7	9446		10720	27275	
DFAFADLTVVYREGN		>18001.8	9627	4915		17973	39785	
TVVYREGNPFGICKL		>18001.8	>13059.7	13850		16200	48840	
GNPFGICKLCLRFLS		1084	9737	1139		196	6594	
NYSVYGNTLEQTVKK		>56657.22	8614	15587		>25108.23	14326	
KKPLNEILIRCIICQ		1299	965	1870		140	26273	
NEILIRCIICQRPLC		20827	7174	18927		883	>29761.9	
IRCIICQRPLCPQEK		6757	7295	25349		510	15154	
CIVYRDCIAYAACHK		35566	12898	3847		2578	1912	
NTELYNLLIRCLRCQ		259	5674	2449		797	854	
IRCLRCQKPLNPAEK		21581	>9641.87	27591		447	20171	
REVYKFLFTDLRIVY		2263	80	258		203	155	
RIVYRDNNPYGVCIM		3446	119	821		1403	20474	
NNPYGVCIMCLRFLS		7786	4797	6662		207	7258	
EERVKKPLSEITIRC		6877	8919	132		2990	7910	
IRCIICQTPLCPEEK		5461	17444	9766		916	>51020.41	
EIPLIDLRLSCVYCK		47355	6936	656		861	16853	
SCVYCKKELTRAEVY		569	23385	4374		673	3197	
VCLLFYSKVRKYRYY		326	309	61		2343	182	
YYDYSVYGATLESIT		9122	8923	1106		32378	>51020.41	
IRCYRCQSPLTPEEK		6645	>14403.29	480		28659	>51020.41	
VYDFVFADLRIVYRD		12168	79	855		4392	>51020.41	
DFVFADLRIVYRDGN		6957	162	1253		6709	8433	
RIVYRDGNPFAVCKV		174	122	81		1606	3148	
GNPFAVCKVCLRLLS		296	7389	117		126	657	
KKCLNEILIRCIICQ		7579	731	3176		257	>9925.56	
NEILIRCIICQRPLC		16056	10184	8177		372	>22909.51	
RTAMFQDPQERPRKL		1034	17086	73192		20481	7474	
LFVVYRDSIPHAACH		1582	697	437		3580	7854	
LTIVYRDDTPHGVCT		15880	1852	27048		16993	>15267.18	
LCIVYRDCIAYAACH		9886	5662	2269		2881	9738	
YKFLFTDLRIVYRDN		10122	77	2912		1342	800	
YNFACTELKLVYRDD		11615	10167	3082		12866	1673	
LKLVYRDDFPYAVCR		698	699	1877		3828	9156	
YDFVFADLRIVYRDG		6540	8173	25727		10907	11161	
LRIVYRDGNPFAVCK		109	123	169		1566	6820	
HEYMLDLQPETTDLY		>56179.78	12990	30895		2099	>22909.51	
TLRLCVQSTHVDIRT		17613	932	3957		243	>22909.51	
IRTLEDLLMGTLGIV		1156	789	2181		23	12385	
LEDLLMGTLGIVCPI		8514	1693	229		1800	9475	
DLLMGTLGIVCPICS		>56179.78	1053	1427		4123	16198	
KATLQDIVLHLEPQN		25948	603	6968		159	>9925.56	
IDGVNHQHLPARRAE		>56179.78	>11475.41	>36842.11		344	12573	
LRAFQQLFLNTLSFV		106	1.01	20		2.2	253	
FQQLFLNTLSFVCPW		10311	9.3	24792		309	17330	

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
QDYVLDLQPEATDLH		>11918.95	>11475.41	>62758.62		1851	>22909.51	
DIRILQELLMGSFGI		18982	5796	1625		16	>55096.42	
IRILQELLMGSFGIV		7978	1038	294		17	>55096.42	
ELLMGSFGIVCPNCS		>59171.6	933	1928		206	>55096.42	
KEYVLDLYPEPTDLY		>59171.6	>14767.93	3171		476	>55096.42	
LRTIQQLLMGTVNIV		3641	6.4	265		15	32108	
IQQLLMGTVNIVCPT		11062	9.0	2010		166	>55096.42	
QLLMGTVNIVCPTCA		>59171.6	118	>38396.62		11550	>55096.42	
RETLQEIVLHLEPQN		7896	11360	16220		95	>55096.42	
LRTLQQLFLSTLSFV		208	55	29		3.1	1994	
LQQLFLSTLSFVCPW		11693	133	296		22	36943	
KDYILDLQPETTDLH		>17436.79	23654	>37448.56		490	>55096.42	
LRTLQQMLLGTLQVV		907	616	1697		88	>46620.05	
LQQMLLGTLQVVCPG		>31645.57	395	1266		1014	29198	
QMLLGTLQVVCPGCA		>31645.57	874	4144		258	>31446.54	
VPTLQDVVLELTPQT		>31645.57	14985	12263		1000	>31446.54	
LQDVVLELTPQTEID		>31645.57	1145	>33090.91		1116	>31446.54	
QDVVLELTPQTEIDL		>31645.57	10274	>33090.91		1719	>31446.54	
CKFVVQLDIQSTKED		>31645.57	>11437.91	22851		301	>31446.54	
VVQLDIQSTKEDLRV		7353	708	5044		226	8690	
DLRVVQQLLMGALTV		667	57	132		9.5	10879	
LRVVQQLLMGALTVT		314	8.9	56		7.7	8755	
VQQLLMGALTVTCPL		11074	574	526		204	7151	
QQLLMGALTVTCPLC		7657	1223	4461		1470	>31446.54	
QLLMGALTVTCPLCA		>31645.57	1817	3761		2224	>31446.54	
REYILDLHPEPTDLF		4152	13183	>33090.91		316	>31446.54	
TCCYTCGTTVRLCIN		8636	739	3820		891	16033	
VRTLQQLLMGTCTIV		1409	37	1829		139	>15267.18	
LQQLLMGTCTIVCPS		9447	753	2441		2667	>15267.18	
MLDLQPETTDLYCYE		>15209.13	>12027.49	>48404.26		20	>15267.18	
VLDLYPEPTDLYCYE		>15209.13	>12027.49	21591		18	>15267.18	
LREYILDLHPEPTDL		9827	12365	10949		2040	>40404.04	
HIEFTPTRTDTYACRV		200000			>7142.86		200000	
LWWVNNESLPVSPRL								
YEEYVRFDSDVGE		200000					200000	
EEYVRFDSDVGE		200000					200000	
APPRLICDSRVLERY		>1111111.11	149	1384	1617	2840	6087	
ICDSRVLERYLLEAK		2945	20402	85	16159	8550	7295	
VLERYLLEAKEAENI		17227	881	269	340	8920	6714	
EHCSLNENITVPDTK		>1111111.11	84	12013	8307	52943	6626	
NENITVPDTKVNFYA		17921	9338	22568	>38167.94	>38461.54	12214	
VPDTKVNFYAWKRME		8861	14795	333	>38167.94	23602	449	
VNFYAWKRMEVGQQA		50	14798	1194	22507	1490	455	
WKRMEVGQQAVEVWQ		512	159	1812	>42194.09	238	4300	

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
VGQQAVEVWQGLALL		>17241.38	1313	12	>38167.94	3901	>7785.13	
VEVWQGLALLSEAVL		5157	4473	58	>38167.94	1334	13794	
GLALLSEAVLRGQAL		2578	1216	1939	>38167.94	3.5	105	
SEAVLRGQALLVNSS		3484	7.4	151	3997	23	1057	
RGQALLVNSSQPWEP		7698	3.4	2876	6165	1554	558	
LVNSSQPWEPLQLHV		>8163.27	504	2359	18044	3412	10039	
QPWEPLQLHVDKAVS		8897	695	12480	1924	103	2929	
LQLHVDKAVSGLRSL		910	53	2707	1044	31	76	
DKAVSGLRSLTTLLR		52	187	60	3150	2006	104	
GLRSLTTLLRALGAQ		3.7	871	6.2	12947	283	2.7	
TTLLRALGAQKEAIS		860	1512	89	33256	251	21	
ALGAQKEAISPPDAA		4212	>12411.35	14216	>91743.12	27294	3963	
KEAISPPDAASAAPL		601	9272	1201	27203	2988	310	
PPDAASAAPLRTITA		2582	10205	1267	10584	182	1117	
SAAPLRTITADTFRK		3883	809	858	2111	17	45	
RTITADTFRKLFRVY		166	95	35	672	1561	93	
DTFRKLFRVYSNFLR		11	10	0.95	43687	1029	26	
LFRVYSNFLRGKLKL		173	80	2.8	8981	2333	2.9	
SNFLRGKLKLYTGEA		192	4730	30	4075	2442	5.7	
KLKLYTGEACRTGDR		>17241.38	880	130	17787	20089	636	
APPRLITDSRVLERY		2750	92	238	710	2263	698	
ITDSRVLERYLLEAK		5279	>14705.88	18	>42194.09	12401	621	
EHTSLNENITVPDTK		>408163.27	13	11082	>42194.09	>29029.03	5547	
KLKLYTGEATRTGDR		4364	841	18	5298	14838	731	
PQPFRPQQPYPQ						15		
PFRPQQPYPQ						42		
PQPFRPQQPYP						14		
PQPFRPQQP						19		
KQPFRPQQPYPQ						56		
PKPFRPQQPYPQ						3.4		
PQPFKPQQPYPQ						19		
PQPFRKQQPYPQ						22		
PQPFRPQKPYPQ						22		
PQPFRPQQPKPQ						325		
PQPFRPQQPYKQ						35		
PQPFRPQQPYPK						22		
QFLGQQQPFPPQ						2.8		
FLGQQQPFPPQ						31		
LGQQQPFPPQ						151		
QFLGQQQPFPP						2.3		
QFLGQQQPF						5.3		
IRNLALQTLPAMCNVY						1.9		
NLALQTLPAMCNVY						27		
LALQTLPAMCNVY						153		
IRNLALQTLPAM						2.0		
IRNLALQTLP						3.0		

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
EGDAFELTVSCQGGLP K								
ESTGMTPEKVPVSEVM GT			>17500			>64444.4 4		
FPTIPLSRLFDNASL		30675	7495	1390	2585	194	5799	
RLFDNASLRAHRLHQ		12461	84	85	11411	3210	557	
LRAHRLHQLAFDTYQ		3208	7590	90	19811	2.0	4471	
QLAFDTYQEFEEAYI		>15384.62	15167	23166	595	11495	>38610.04	
QEFEEAYIPKEQKYS		12821	>15837.1	>15582.1 9	>54554.47	>41134.7 5	5418	
IPKEQKYSFLQNPQT		>15384.62	13695	16207	30572	55587	13118	
SFLQNPQTSLCFSES		>15384.62	190	6513	93809	21651	>9647.76	
TSLCFSESIPTPSNR		>15384.62	99	1944	3920	1883	>38610.04	
REETQQKSNLELLRI		>15384.62	15709	9736	>270270.27	52	25133	
SNLELLRISLLLIQS		23669	196	59	>91901.83	147	50110	
ISLLLIQSWLEPVQF		2675	120	60	6765	2.5	>9960.16	
SWLEPVQFLRSVFAN		2715	4322	136	>270270.27	291	4815	
FLRSVFANSLVYGAS		973	5.6	13	157978	814	141	
NSLVYGASDSNVYDL		>15384.62	14038	3640	11769	1792	>13046.31	
SDSNVYDLLKDLEEG		>15384.62	>17857.14	>30536.9 1	219298	>137767. 22	>13046.31	
GIQTLMGRLEDGSPR		4474	10433	1348	186220	2110	18006	
RLEDGSPRTGQIFKQ		7896	>17857.14	9106	18119	296	12580	
RTGQIFKQTYSKFDT		6961	66	155	14736	201	64	
QTYSKFDTNSHNDDA		>15384.62	>17857.14	25883	38715	>137767. 22	5787	
TNSHNDDALLKNYGL		>15384.62	5169	133	130378	>137767. 22	>13046.31	
ALLKNYGLLYCFRKD		>15384.62	10	17	2309	1230	462	
DMDKVETFLRIVQCR		885	1232	201	>27322.4	826	7447	
FLRIVQCRSVEGSCGF		2708	1017	839	>27322.4	1078	7102	
FPTIPLSRLFDNAML		46404	9313	2770	121212	216	11521	
RLFDNAMLRAHRLHQ		267	738	18	>270270.27	1628	58	
QLAFDTYQEFEQNPQ		>15384.62	19718	>86666.6 7	738	>32842.5 8	>9510.22	
SFLQNPQTSLCCFRK		3801	128	103	>270270.27	8500	3739	
SNLELLRICLLLIQS		>15384.62	773	90	17024	164	>11771.33	
ICLLLIQSWLEPVQF		>15384.62	954	1771	187970	49	>9510.22	
NSLVYGASDSNIYDL		>15384.62	10854	971	31616	3287	>9510.22	
SDSNIYDLLKDLEEG		>15384.62	>16203.7	>86666.6 7	>18726.59	24259	>9510.22	
DKVETFLRIVQCCGF		1023	1034	383	6278	184	6350	
SFLQNPQTSLTFSES		>15384.62	121	1511	864	17824	12365	
TSLTFSESIPTPSNR		22152	16	176	>95238.1	3476	>1335.38	
ALLKNYGLLYTFRKD		1737	0.89	6.5	50	1335	29	
LLYTFRKDMDKVETF		7905	>14522.82	886	941	12493	154	
DMDKVETFLRIVQTR		206	3381	>86666.6 7	13712	190	1263	
FLRIVQTRSVEGSTGF		143	1.5	9.8	27345	21	116	
HLDMLRHLYQGCQVV		2076	2879	359	107066	163	7087	
RLRIVRGTQLFEDNYAL		2072	5.2	31	1198	120	46	
GVGSPYVSRLLGICL		696	955	46	148588	316	14197	
TLERPKTLSPGKNGV		>52631.58	835	23264	>263157.89	25739	11337	

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
KIFGSLAFLPESFDGDP A		>52631.58	1073	2264	43745	10020	8008	
ELVSEFSRMARDPQ		4573	>71428.57	7891	15838	970	4055	
GEALSTLVLNRLKVG		79	29	269		1023	46	
AYVLLSEKKISSIQS		51	816	489		902	4517	
VASLLTTAEVVVTEI		>18674.14	>10294.12	>50837.9 9		>26435.7 3	>119047.6 2	
KCEFQDAYVILLSEKK		1078	>10294.12	>47643.9 8		>19594.5 9	20	
ALSTLVLNRLKVGLQ		9.1	4.6	191		17	3.9	
MSYNLLGFLQRSSNC		3628	1190	89	>42194.09	6503	710	
LGFLQRSSNCQCQKL		6025	112	1397	>42194.09	1167	649	
RSSNCQCQKLLWQLN		>408163.27	6153	802	3519	21	6981	
QCQKLLWQLNGRLEY		1644	227	175	8709	209	924	
LWQLNGRLEYCLKDR		4215	808	893	29028	15576	3241	
GRLEYCLKDRRNFDI		1707	1240	940	5213	15870	64725	
RNFDIPEEIKQLQQF		7326	>15418.5	2036	23832	311	6854	
PEEIKQLQQFQKEDA		1953	13325	1873	>26315.79	215	675	
QLQQFQKEDAAVTIY		>408163.27	68	1724	348	1338	4270	
QKEDAAVTIYEMLQN		>408163.27	7315	1146	>42194.09	15173	>10482.18	
AVTIYEMLQNIFAIF		29718	109	262	2828	1118	14047	
EMLQNIFAIFRQDSS		36832	61	1718	726	164	3187	
IFAIFRQDSSSTGWN		4558	775	204	2181	30	109290	
RQDSSSTGWNETIVE		>42553.19	848	>189583. 33	9172	1497	8650	
STGWNETIVENLLAN		20576	105	897	>26315.79	166	5822	
ETIVENLLANVYHQR		>42553.19	8.5	1603	>42194.09	2503	18559	
NLLANVYHQRNHLKT		8258	61	20	>123456.79	3071	65	
VYHQRNHLKTVLEEK		22002	1267	1662	>123456.79	9585	4.7	
LEKEDFTRGKRMSSL		698	25362	14118	6267	16057	4903	
FTRGKRMSSLHLKRY		81	10245	118	18836	2027	84	
RMSSLHLKRYYGRIL		1035	2532	1.3	>26178.01	2255	491	
HLKRYYGRILHYLKA		2721	868	0.69	6608	22	2.3	
YGRILHYLKAKEDSH		812	2783	16	454545	140	39	
HYLKAKEDSHCAWTI		>60606.06	11571	627	301205	7501	2632	
KEDSHCAWTIVRVEI		9320	506	1397	>1754385.9 6	7.9	4056	
CAWTIVRVEILRNFY		4167	147	196	10300	152	4143	
VRVEILRNFYVINRL		504	5.8	1.04	80386	187	485	
RNFYVINRLTGYLRN		55	9.4	18	689	1249	5.6	
MSYNLLGFLQRSSNT		3069	1334	6.8	51787	4660	9.0	
LGFLQRSSNTQTQKL		26247	21	2331	>1754385.9 6	1041	339	
RSSNTQTQKLLWQLN		>42553.19	169	2740	751	26	8545	
QTQKLLWQLNGRLEY		20654	121	20	6582	88	417	
LWQLNGRLEYTLKDR		6521	2447	853	4402	14310	6004	
GRLEYTLKDRRNFDI		4998	1468	168	9901	21427	796	
HYLKAKEDSHTAWTI		>60606.06	2264	529	35829	11750	19617	
KEDSHTAWTIVRVEI		7443	3046	1992	56205	18	575	
TAWTIVRVEILRNFY		5052	72	242	14419	26	518	
LGFLQRSSNCQSQKL		604	131	541	>1754385.9	124	508	

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
RSSNCQSQKLLWQLN		>60606.06	1960	2962	68823	27	4077	
QSQKLLWQLNGRLEY		>60606.06	155	108	5609	166	402	
GIVEQCCTSICSLYQ		7940	239	1280	14353	4245	>37593.98	
TSICSLYQLENYCN		>10526.32	>15021.46	837	8048	13496	>40322.58	
GILEQCCTSICSLYQ		>10526.32	858	1097	>18726.59	5871	19231	
GIVEQTTTSITSLYQ		>10526.32	14	849	>95238.1	2303	>37593.98	
EQTTTSITSLYQLEN		>10526.32	16949	1078	>18726.59	29614	48505	
TSICSLYQLENYCG		>10526.32	10346	173	>95238.1	1645	>40322.58	
TSITSLYQLENYTN		1095	>17073.17	99	>95238.1	3245	6048	
TSITSLYQLENYTG		1014	>17073.17	182	92336	1658	16073	
GIVEQCCCGSHLVEA		>10526.32	15347	237	14184	11017	>43290.04	
SLYQLENYCCGERGF		>1111111.11	>15909.09	151	92336	30978	>43290.04	
CCTSICSLYQLENYCC		>1111111.11	7096	877	>18726.59	1582	>40650.41	
GSHLVEALYLVCCN		>1111111.11	3259	11191	>18726.59	14065	>46403.71	
CCGSHLVEALYLVCC		>10526.32	6027	12986	>18726.59	11357	>43290.04	
FVNQHLCGSHLVEAL		>1111111.11	10595	1195	>95238.1	3153	47170	
QHLCGSHLVEALYLV		>10526.32	7624	103	14819	1480	32049	
GSHLVEALYLVCGER		>10526.32	8030	1350	>18726.59	372	29283	
VEALYLVCGERGFFY		3563	4403	181	4443	30	25543	
YLVCGERGFFYTPKT		>10526.32	9272	10655	92764	34450	95238	
FVNQHLCGSDLVEAL		>1111111.11	20248	9679	10031	24511	>43290.04	
FVNQHLTGSHLVEAL		>10526.32	12413	799	94518	4084	>43290.04	
QHLTGSHLVEALYLV		>10526.32	6862	184	4027	939	23716	
GSHLVEALYLVTGER		>10526.32	12185	1429	18215	225	11398	
VEALYLVCGERGSFY		>10526.32	4288	1240	>95238.1	129	804	
VEALYLVCGERGFLY		55402	1871	149	843	19	5149	
VEALYLVTGERGFFY		4860	1076	116	17156	13	78	
YLVCGERGFLYTPKT		>1111111.11	2120	>25633.8	>95238.1	33114	971	
YLVCGERGFFYTDKT		>60606.06	1014	>25633.8	616	48099	>28449.5	
YLVCGERGFFYTKPT		>60606.06	3467	>25633.8	12805	40379	>28449.5	
YLVTGERGFFYTPKT		7625	2100	>25633.8	13737	20721	>28449.5	
YLVTGERGFFYTDKT		16849	17353	>25633.8	359	30824	>28449.5	
YLVTGERGFFYTKPT		9341	17869	>21016.17	9573	27915	11926	
VCGERGFFYTPKTRR		3817	34669	>25633.8	17416	>30999.47	92	
VTGERGFFYTPKTRR		10116	25362	2824	243902	>29820.05	540	
MWDLVLSIALSVGCT		81096	108	11375	15205	158	70711	
DLVLSIALSVGCTGA		>200000	98	18200	>14918.69	459	>100000	
HPQWVLTAAHCLKKN		981	483	1219	8114	1106	11	
QWVLTAAHCLKKNSQ		14213	>35000	>45500	>14918.69	14395	382	
GQRVPVSHSFPHPLY		>200000	703	3960	>14918.69	9860	>200000	
RVPVSHSFPHPLYNM		>200000	377	5518	>14918.69	9213	11650	
PHPLYNMSLLKHQSL		6455	3307	3873	>14918.69	49	1901	
HPLYNMSLLKHQSLR		248	546	472	>14918.69	8.4	219	
NMSLLKHQSLRPDED		25820	>35000	>30333.33	>14918.69	105	>100000	

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
SHDLMLLRLSEPAKI		5267	1.8	365	5361	10	2031	
HDLMLLRLSEPAKIT		1147	0.83	115	488	12	211	
PEEFLRPRSLQCVSL		10675	11667	3193	>14413.38	117	57537	
PRSLQCVSLHLLSND		11128	3731	1597	11650	544	46416	
NGVLQGITSWGPEPC		32444	>17500	835	>14413.38	5761	>100000	
KPAVYTKVVHYRKWI		327	1947	401	7186	4581	23	
LHLLSNDMCARAYSE		26012	1876	>2367.33	1308	324	28817	
VGNWQYFFPVIFSKA								
ESEFQAALSRKVAKL								
IGHLYIFATCLGLSYDG L								
VGNWQYFFPVIFSKAS DSLQLVFGIELMEVD PAYEKLSAEQSPPPY								
RNGYRALMDKSLHVG TQCALTRR								
FFKNIVTFFKNIVT								
YKSAHKGFKGVDAQG TLSKI		2000					1333	2065
VDAQGTLSKIFKLGGR DSRS		18			769		6667	1152
AC-ASQKRPSQRHGSKYLA TAST		200000					200000	4561
ENPVVHFFKNIVTPR				5.2			463	
ENPVVAFFKNIVTPR				2.8			302	
ENPVVHAFKNIVTPR				4.1			910	
ENPVVHFFANIVTPR				2.9			6235	
ENPVVHFFKNIVTPA				2.5			3333	
NPVVHFFKNIVT				23			10000	
HFFKNIVTPRTPPY				460			377	
NPVVHFFKNIVTPR				3.7			1890	
LPVPGVLLKEFTVSGNI LTI		216	52	84		349	1840	
WITQCFLPVFLAQPPSG QRR		13208	23649	726		688	286	
DHRQLQLSISSCLQQLS LLM		>98522.17	69	67		532	63772	
YLAMPFATPMEAELAR RSLA		3754	2813	865		1965	641	
AAPLLLARAASLSLG		100	3.2	35	10470	79	79	
APLLLARAASLSLGF		322	12	91	13359	59	114	
PLLLARAASLSLGFL		1255	12	118	>9742.79	52	151	
SLSLGFLFLLFFWLD		100000	639	11375	3710	>10955.8	66667	
LLFFWLDRSVLAKEL		154	24	34	86	7.5	134	
DRSVLAKELKFVTLV		20966	4410	1359	>14413.38	53	2217	
AKELKFVTLVFRHGD		12309	824	1529	8563	51	24	
RSPIDTFPTDPIKES		>200000	>35000	2373	>14413.38	469	28571	
FGQLTQLGMEQHYEL		27217	>35000	>22750	>14413.38	543	100000	
DRTLMSAMTNLAALF		2367	114	871	3927	57	26138	
MSAMTNLAALFPPEG		>200000	249	12384	7158	1072	63246	
MTNLAALFPPEGVSI		141421	1310	10370	>8829.24	4606	141421	
PEGVSIWNPILLWQP		30861	444	7.2	4624	107	22222	
GVSIWNPILLWQPIP		10287	207	5.0	4428	492	523	

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
WNPILLWQPIPVHTV		19640	2259	14	>8829.24	81	100000	
NPILLWQPIPVHTVP		599	250	4.6	>8829.24	67	25000	
PILLWQPIPVHTVPL		4041	567	6.9	>8829.24	106	41491	
ILLWQPIPVHTVPLS		2343	1111	65	>8829.24	712	28768	
WQPIPVHTVPLSEDQ		>66666.67	2692	>45500	>8829.24	1228	>100000	
LSGLHGQDLFGIWSK		30151	>35000	32173	>8829.24	135	81650	
YDPLYCESVHNFTLP		30151	>35000	2136	>8829.24	6901	28768	
LPSWATEDTMTKLRE		>66666.67	>35000	>45500	5973	>11134.57	343	
LRELSELSLLSLYGI		6958	3218	235	>14956.63	544	5185	
LSELSLLSLYGIHKQ		1657	1253	45	>13046.31	79	7.3	
LSLLSLYGIHKQKEK		742	>35000	58	>14956.63	772	3.4	
KSRLQGGVLVNEILN		>66666.67	318	>30333.33	>14956.63	713	>100000	
GGVLVNEILNHMKRA		255	49	576	8124	5.8	8.7	
IPSYKKLIMYSAHDT		53	2122	17	9982	12	191	
YKKLIMYSAHDTTVS		208	37	15	13224	5.8	5482	
LIMYSAHDTTVSGLQ		>66666.67	1752	184	6828	4381	>100000	
DTTVSGLQMALDVYN		>50000	3500	1042	10843	961	>200000	
ALDVYNGLLPPYASC		182	>35000	1091	>14956.63	>10090.47	115470	
LDVYNGLLPPYASCH		194	>35000	3035	>14956.63	>10918.67	25820	
YNGLLPPYASCHLTE		5300	11667	252	>14956.63	>10918.67	100000	
FAELVGPVIPQDWST		>50000	>35000	>45500	>14956.63	983	>200000	
TVPLSEDQLLYLPFR		26455	5300	>2367.33	4323	872	27221	
LTELYFEKGEYFVEM		>18903.59	3157	>2367.33	124	601	6655	
GPVIPQDWSTECMTT					20295	961		
QAHSLERVCHCLGKWLGHPDK		2857					2500	
WTTCQSIAFPSKTSASIGSL		40000		277	37450	505	400	
QKGRGYRGQHQAHSLERVCH		30151		>9100	>500000	17951	9759	
AATYNFAVLKLMGRGTKF		17		239	70014	1218	18	
VATGLCFFGVALFCGCGHEA		33333			117851	193333		
FLYGALLLAEGFYTTGAVRQ				45			256	
SAVPVYIYFNTWTTCQSIAF				92			20000	
TLSVTWIGAAPLILS		6860	642	97	6031	3506	31	
SVTWIGAAPLILSRI		2196	420	147	13676	42	104	
VTWIGAAPLILSRIV		1779	2339	552	>10729.61	88	147	
SQPWQVLVASRGRAV		135	32	11259	>12116.81	7562	84	
GRAVCGGVLVHPQWV		>50000	5456	12888	>12116.81	62	100000	
GVLVHPQWVLTAAHC		263	2427	66	>10729.61	6.2	1062	
HPQWVLTAAHCIRNK		785	1170	6500	1324	5518	40	
QWVLTAAHCIRNKSV		2169	2062	13565	7342	3802	35	
AHCIRNKSVILLGRH		93	75	88	4752	8.7	3630	
SVILLGRHSLFHPED		96	96	106	13045	4411	16116	
VILLGRHSLFHPEDT		344	543	426	>12116.81	10696	100000	
GQVFQVSHSFPHPLY		103	146	2172	1071	416	128	

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
VFQVSHSFPHPLYDM		881	83	2396	23433	>12491.92	897	
PHPLYDMSLLKNRFL		>50000	11667	712	>13533.63	7486	3104	
SHDLMLLRLSEPAEL		4471	5.8	1099	13577	12	100000	
HDLMLLRLSEPAELT		2141	2.3	662	5305	45	10541	
TDAVKVMDLPTQEPA		>50000	>35000	>45500	>13533.63	747	>200000	
LHVISNDVCAQVHPQ		>50000	239	22750	1887	1087	>200000	
CAQVHPQKVTKFMLC		18490	2192	809	>13533.63	604	1229	
GGPLVCNGVLQGITS		1828	36	30333	>6567.28	815	13417	
GPLVCNGVLQGITSW		915	49	6310	11615	646	6537	
NGVLQGITSWGSEPC		9724	775	258	8038	4487	11619	
RPSLYTKVVHYRKWI		350	4183	717	2982	4897	13	
HSLFHPEDTGQVFQV					553	11503		
PRWLCAGALVLAGGF		>40000	20207	15167	13150	883	40825	
LGFLFGWFIKSSNEA		7303	10104	355	681	9285	461	
LDELKAENIKKFLYN		324	597	414	548	788	150	
IKKFLYNFTQIPHLA		137	27	305	477	96	658	
KFLYNFTQIPHLAGT		91	221	227	10212	256	1600	
WKEFGLDSVELAHYD		4935	8413	22750	829	5925	89443	
LAHYDVLLSYPNKTH		380	268	82	1406	589	172	
GNEIFNTSLFEPPPP		>40000	2804	>91000	>13164.82	835	>200000	
GKVFRGNKVKNAQLA		894	46	3373	7591	7884	1385	
GNKVKNAQLAGAKGV		>66666.67	>35000	>45500	>12462.61	1065	1218	
EYAYRRGIAEAVGLP		2590	5217	>45500	8773	6325	1204	
AEAVGLPSIPVHPIG		>66666.67	5456	56	>11848.34	12394	69336	
AVGLPSIPVHPIGYY		33333	1191	518	>11848.34	5387	38517	
IGYYDAQKLLEKMGG		>28571.43	5729	1978	17305	13588	506	
TGNFSTQKVKMHIHS		11856	6187	3745	>11848.34	508	1927	
TRIYNVIGTLRGAVE		45	1460	1605	17550	447	32	
ERGVAYINADSSIEG		>50000	3689	30333	6846	87	200000	
GVAYINADSSIEGNY		>40000	497	7610	1420	477	66667	
DSSIEGNYTLRVDCT		>50000	7.6	1202	576	1262	16824	
NYTLRVDCTPLMYSL		7116	9.0	5056	25	404	66667	
CTPLMYSLVHNLTKE		590	260	426	18348	58	36	
DFEVFFQRLGIASGR		128	10069	10249	30745	4.2	3559	
EVFFQRLGIASGRAR		31	17500	4556	>15037.59	51	7.9	
TNKFSGYPLYHSVYE		33333	>35000	489	>21853.15	12466	2942	
YDPMFKYHLTVAQVR		252	1014	1348	8137	553	62	
DPMFKYHLTVAQVRG		69	699	230	7297	467	11	
MFKYHLTVAQVRGGM		147	1615	1198	3648	1062	5.8	
KYHLTVAQVRGGMVF		859	193	1222	>21853.15	3446	86	
VAQVRGGMVFELANS		>50000	2802	117	>21853.15	100	64366	
RGGMVFELANSIVLP		>50000	4.4	94	132	411	413	
GMVFELANSIVLPFD		>50000	12	83	234	4154	903	
VFELANSIVLPFDCR		11765	24	477	128	1215	10815	
ADKIYSISMKHPQEM		169	4957	8273	>21853.15	3550	26726	
IYSISMKHPQEMKTY		213	>35000	5025	>21853.15	5356	2588	

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
PQEMKTYSVSFDSLF		>50000	24749	919	14564	579	100000	
TYSVSFDSLFSAVKN		5981	5888	3223	8547	10461	61	
VLRMMNDQLMFLERA		2353	130	127	98	88	85	
LRMMNDQLMFLERAF		1833	1314	1411	1570	50	758	
RHVIYAPSSHNKYAG		13363	8750	1291	>62814.07	5293	88	
RQIYVAAFTVQAAAE		35	524	166	6808	47	143	
QIYVAAFTVQAAAET		34	344	252	1324	50	216	
VAAFTVQAAAETLSE		2126	446	18200	2116	464	378	
YISIINEDGNEIFNT		>18903.59	346	2713	30	3705	72993	
ISIINEDGNEIFNTS		>18903.59	343	3006	35	6394	>37807.18	
EDFFKLERDMKINCS		10433	3188	>3490.6	4036	7886	3494	
FFKLERDMKINCSGK		9687	382	>3490.6	4918	98	3796	
GVILYSDPADYFAPG		>18903.59	39	965	8.8	64	14168	
GAAVVHEIVRSFGTL					788	89		
NSRLLQERGVAYINA		12812	327	1229	3366	699	3473	
VAYINADSSIEGNYT		>18903.59	2147	>3490.6	471	841	>37807.18	
DQLMFLERAFIDPLG					17115	6.6		
KSNFLNCYVSGFHPSD		5000					2857	
AC-NPDAENWNSQFEILEDAA		>33333.33	>10000	>10000	1000		50000	
EYLILSARDVLAVVS		6860		2340		2527	4154	
YKTIAYDEEARR		200000		>91000	>50000		200000	
GEALSTLVVNKIRGT		977	55	2314		1514	108	
PYILLVSSKVSTVKD		112	7.2	22		107	32	
EAVLEDPYILLVSSK		4376	>10294.12	>50837.99		>26435.73	357	
IAGLFLTTEAVVADK		867	>10294.12	>50837.99		>26435.73	606	
ALSTLVVNKIRGTFK		32	7.6	160		214	38	
MKHILYISFYFILVN		2082					>9523.81	
KSLLSTNLPYGRTNL								
HFFLFLLYILFLVKM			84	21473		1064	10083	
LFLLYILFLVKMNAL			129	30829		1290	32446	
ILFLVKMNALRRLPV			0.13	1.4		7.6	14	
MNALRRLPVICSFLV			15	36		5.7	2557	
SAFLESQSMNKIGDD			52	18689		302	243	
LKELIKVGLPSFENL			147	361		110	41322	
FENLVAENVKPPKVD			3029	>50837.99		9297	62661	
PATYGIIVPVLTSLF			0.83	2557		118	52	
YGIIVPVLTSLFNKV			0.30	223		97	80	
LLKIWKNYMKIMNHL			3.7	6.8		12	35	
MTLYQIQVMKRNQKQ			323	2429		82	22	
QKQVQMMIMIKFMGV			17	363		5.3	915	
MIMIKFMGVIYIMII			102	23611		145	12310	
GVIYIMIISKKMMRK			38	173		157	46	
LYYLFNQHIKKELYH			327	2861		1089	606	
HFNMLKNKMQSSFFM			54	616		934	60	

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
LDIYQKLYIKQEEQK			4346	47		70	6958	
QKKYIYNLIMNTQNK			53	844		87	245	
YEALIKLLPFSKRIR			230	36		15	11	
ENEYATGAVRPFQAA			9302	3007		10026	>10303.97	
NYELSKKAVIFTPIY			410	537		136	10581	
QKILIKIPVTKNIIT			332	3614		953	297	
KCLVISQVSNSDSYK			236	403		81	>42553.19	
SKIMKLPKLPISNGK			6460	3570		6739	>10303.97	
FIHFFTWGTMFVPKY			328	2375		387	9608	
LCNFKKNIIALLIIP			16	29302		99	>42553.19	
KKNIIALLIIPPKIH			15	32		8.2	143	
ALLIIPPKIHISIEL			162	1823		10	7135	
SMEYKKDFLITARKP			3818	4610		10448	442	
KSKFNILSSPLFNNF			25	5.9		135	32	
FKKLKNHVLFLQMMN			20	29		14	59	
KNHVLFLQMMNVNLQ			36	224		22	>7212.41	
VLFLQMMNVNLQKQL			8.6	8200		12	>7212.41	
NVNLQKQLLTNHLIN			28	4448		354	>7212.41	
QKQLLTNHLINTPKI			1.6	514		904	6595	
NHLINTPKIMPHHII			32	560		1632	8882	
YILLKKILSSRFNQM			1.01	26		340	83	
FNQMIFVSSIFISFY			33	3903		1291	>12484.39	
KVSCKGSGYTFTAYQMH		>200000						
IAKVPPGPNITAEYGDKWLD		200000			>20000		200000	
TAEYGDKWLDAKSTWYGKPT		200000			>20000		10000	
AKSTWYGKPTGAGPKDNGGA		200000			>20000		10000	
GAGPKDNGGACGYKDVDKAP		200000			>20000		200000	
FNGMTGCGNTPIFKDGRGCG		200000			>20000		200000	
PIFKDGRGCGSCFEIKCTKP		200000			>20000		200000	
SCFEIKCTKPESCSGEAVTV		200000			>20000		200000	
AFGSMAKKGEEQNVRSAGEL		1818			>33333.33		200000	
TPDKLTGPFTVRYTTEGGTK		200000			>25000		200000	
VRYTTEGGTKSEVEDVIPEG		200000			>25000		200000	
TCVLGKLSQELHKLQ		1398	>12589.93	2009	>263157.89	163	3986	
KLSQELHKLQTYPRT		2375	>12589.93	287	>263157.89	870	37	
LHKLQTYPRTNTGSG		6091	>12589.93	157	>263157.89	22948	40	
KLQTYPRTNTGSGTP		8210	987	520	>263157.89	>104693.14	>14044.94	
CCVLGKLSQELHKLQ		5243	>12589.93	570	>263157.89	346	5158	
CSNLSTCVLGKLSQE		5263	7907	4538	>263157.89	11756	5709	
TSNLSTTVLGKLSQE		534	9333	7697	>263157.89	13210	2529	
TTVLGKLSQELHKLQ		3524	12715	525	>263157.89	241	10618	
DIAAKYKELGY		>10000			>25000		200000	
ALVRQGLAKVA		200000					>10000	

		HLA-DR SUPERTYPE						
Sequence	SEQ ID NO.	DRB1 *1101	DRB1 *1302	DRB1 *1501	DRB3 *0101	DRB4 *0101	DRB5 *0101	DRB5 *0201
PATLIKAIDGDTVKLMY KGQ		>6666.67			2381		3333	
TPETKHPKKGVEKYGP EASA		>6666.67			>25000		>4000	
VEKYGPEASAFTKKMV ENAK		20000			16667		34	
FTKKMVENAKKIEVEF DKGQ		6667			>25000		1000	
YIYADGKMVNEALVRQ GLAK		>6666.67			>5555.56		>4000	
HEQHLRKSEAQAKKEK LNIW		200000			>5555.56		11	
QAKKEKLNIWSEDNAD SGQ		200000			>5555.56		200000	
YFNNFTVSFWLRVPK								
FSYFPSI								
YSFFPSI								
YSYFPSIR		20000					>200000	
DPNANPNVDPNANPNV NANPNANPNANP(X4) QKWAAVVVPS		>12500		>7583.33		>72500	>2898.55	
TWQLNGEELIQDMELV ETRPAG								
PEFLEQRRAAVDTYC		488					200000	
STORKUSP33								
DYSYLQDSDPDSFQD		>66666.67	>35000	>45500			>40000	
DFSYLQDSDPDSFQD			>35000	>91000			>40000	
QNILFSNAPLGPQFP								
QNILLSNAPLVPQFP								
DYSYLQDSDPDSFQD								
KYVKQNTLKLAT								
P(X)KQNTLKLAT								
EEDIEIIPIQEEEY		>20576.13					46083	
HQAISPRTLNSPAIF		33686	1036	8106	>83333.33	130	>200000	
YTDVFSLDPTFTIETT								
YAGIRRDGLLLRLVD								
LFFYRKSVWSKLQSI		12	121	20	5915	1933	18	
RPIVNMDYVVGARTFR REKR		222	73	43	3324	160	6.6	
RPGLLGASVLGLDDI		>93896.71	2056	6000	30212	22038	>88888.89	
LYFVKVDVTGAYDTI		221	79	9753	16	22	4962	
FAGIRRDGLLLRLVD		804	1294	28	553	1670	1355	
AKTFLRTLVRGVPEY		6.3	94	829	546	472	3484	
YGAVVNLRKTVVNFP		89	11236	470	51496	302	36	
GTAFVQMPAHGLFPW		17	2819	1.2	769	2361	43	
WAGLLLDTRTLEVQS		20960	92	3468		862	>102040.8 2	
RTSIRASLTFNRGFK		4807	49	497		79	52	
RVIKNSIRLTL		1740	32	4317		143	8834	
PVIKNSIKLRL		2772	77	2579		198	1039	
ATSTKKLHKEPATLIKA IDG		>6666.67			462		267	

TABLE 28

MURINE CLASS I SUPERTYPE

Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
SGPSNTPPEI		10	Adenovirus	E1A		
RNPRFYNL		8	Artificial sequence	Consensus		
QPQRGYENF		9	Artificial sequence	Consensus		A
SEAAYAKKI		9	Artificial sequence	pool consensus		A
AYAPAKAAI		9	Artificial sequence			Poly
AYAEAKAAI		9	Artificial sequence			Poly
AYANAKAAI		9	Artificial sequence			Poly
AYAGAKAAI		9	Artificial sequence			Poly
AYAVAKAAI		9	Artificial sequence			Poly
AAAAYAAM		8	Artificial sequence			
AAAAYAAAAM		10	Artificial sequence			
AAAANAAAM		9	Artificial sequence			
AAAAAANAAAM		11	Artificial sequence			
NAIVFKGL		8	Chicken	Ova	176	
SIINFEKL		8	Chicken	Ova	257	
IFYCPIAI		8	Chicken	Ova	27	
KVVRFDKL		8	Chicken	Ova	55	
VYSFSLASRL		10	Chicken	Ova	96	
SIINFEKL		8	Chicken	Ova	257	
KVVRFDKL		8	Chicken	Ova	55	
SENDRYRLL		9	EBV	BZLF1	209	A
SFYRNLLWL		9	Flu	HA	142	
YEANGNLI		8	Flu	HA	259	A
MGLIYNRM		8	Flu	M1	128	
MGYIYNRM		8	Flu	M1	128	
MGIIYNRM		8	Flu	M1	128	
MGLIFNRM		8	Flu	M1	128	
MGLIYNRM		8	Flu	M1	128	
RMIQNSLTI		9	Flu	NP	55	
RLIQNFLTI		9	Flu	NP	55	
GMRQNATEI		9	Flu	NP	17	
YMRVNGKWM		9	Flu	NP	97	
FYIQMATEL		9	Flu	NP	39	
FYIQMCTFL		9	Flu	NP	39	
AYERMANIL		9	Flu	NP	218	
AYQRMCNIL		9	Flu	NP	218	
AYERMCTIL		9	Flu	NP	218	
ASNENMETM		9	Flu	NP	366	
TYQRTRALM		9	Flu	NP	147	A
TYQKTRALV		9	Flu	NP	147	A
TYQPTRALV		9	Flu	NP	147	A
TYQFTRALV		9	Flu	NP	147	A
TYQLTRALV		9	Flu	NP	147	A
SDYEGRLI		8	Flu	NP	50	
MITQFESL		8	Flu	NS	31	
RTFSFQLI		8	Flu	NS	114	
FSVIFDRL		8	Flu	NS	134	

MURINE CLASS I SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
RTFSFQLI		8	Flu	NS1	114	
MITQFESL		8	Flu	NS1	31	
FSVIFDRL		8	Flu	NS2	134	
KSSFYRNL		8	FluA	HA	158	
SSLPFQNI		8	FluA	HA	305	
MNIQFTAV		8	FluA	HA	403	
MNYYWTLL		8	FluA	HA	244	
SFYRNLLWL		9	FluA	HA	160	
SSLPFQNI		8	FluA	HA	305	
MNIQFTAV		8	FluA	HA	403	
MNYYWTLL		8	FluA	HA	244	
KSSFYRNL		8	FluA	HA	158	
SIIPSGPL		8	FluA	M1	13	
LSYSAGAL		8	FluA	M1	117	
LSYSAGAL		8	FluA	M1	117	
SSISFCGV		8	FluA	NM	426	
TGICNQNII		9	FluA	NM	46	
ITYKNSTWV		9	FluA	NM	54	
FCGVNSDTV		9	FluA	NM	430	
TGICNQNII		9	FluA	NM	46	
FCGVNSDTV		9	FluA	NM	430	
ITYKNSTWV		9	FluA	NM	54	
SSISFCGV		8	FluA	NM	426	
IGRFYIQM		8	FluA	NP	36	
MMIWHSNL		8	FluA	NP	136	
ASNENMETM		9	FluA	NP	366	
IGRFYIQM		8	FluA	NP	36	
MMIWHSNL		8	FluA	NP	136	
FFYRYGFV		8	FluA	POL1	495	
KMITQRTI		8	FluA	POL1	198	
RSYLIRAL		8	FluA	POL1	215	
RFYRTCKL		8	FluA	POL1	465	
TALANTIEV		9	FluA	POL1	141	
TALANTIEV		9	FluA	POL1	141	
RSYLIRAL		8	FluA	POL1	215	
RFYRTCKL		8	FluA	POL1	465	
VYINTALL		8	FluA	POL2	463	
VYINTALL		8	FluA	POL2	463	
VYIEVLHL		8	FluA	POL3	227	
VYIEVLHL		8	FluA	POL3	227	
WYIPPSLRTL		10	GAD			
MURTAZAKDPEPTIDES		0	GAD65		107	
IYSTVASSL		9	HA		553	
LYEKVKSQL		9	HA		462	
LYQKVKSQL		9	HA		462	
LYEKMKSQL		9	HA		462	
LYEKVFSQL		9	HA		462	
LYQNVGTYV		9	HA		204	

MURINE CLASS I SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
MGLKFRQL		8	HBV	core	122	
VSYVNTNM		8	HBV	core	115	
SYVNTNMGL		9	HBV	core	116	
MGLKFRQL		8	HBV	core	122	
VSYVNTNM		8	HBV	core	115	
SYVNTNMGL		9	HBV	core	116	
WGPSLYSI		8	HBV	env	364	
ASARFSWL		8	HBV	env	329	
WGPSLYSIL		9	HBV	env	364	
TGPCRTCMT		9	HBV	env	281	
WYWGPSLYSI		10	HBV	env	362	
IPQSLDSWWTSL		12	HBV	env	28	
IPQSLDSYWTSL		12	HBV	env	28	A
ASARFSWL		8	HBV	env	329	
WYWGPSLYSI		10	HBV	env	362	
APQSLDSWWTSL		12	HBV	env	28	
IPQALDSWWTSL		12	HBV	env	28	A
IPQSLASWWTSL		12	HBV	env	28	A
IPQSLDAWWTSL		12	HBV	env	28	A
IPQSLDSAWTSL		12	HBV	env	28	A
IPQSLDSWWASL		12	HBV	env	28	A
IPQSLDSWWTAL		12	HBV	env	28	A
EPQSLDSWWTSL		12	HBV	env	28	A
IPESLDSWWTSL		12	HBV	env	28	A
IPQSLDEWWTSL		12	HBV	env	28	A
IPQSLDSWWTEL		12	HBV	env	28	A
RPQSLDSWWTSL		12	HBV	env	28	A
IPRSLDSWWTSL		12	HBV	env	28	A
IPQRLDSWWTSL		12	HBV	env	28	A
IPQSRDSWWTSL		12	HBV	env	28	A
IPQSLRSWWTSL		12	HBV	env	28	A
IPQSLDRWWTSL		12	HBV	env	28	A
IPQSLDSRWTSL		12	HBV	env	28	A
IPQSLDSWWRSL		12	HBV	env	28	A
IPQSLDSWWTRL		12	HBV	env	28	A
YPQSLDSWWTSL		12	HBV	env	28	A
IPYSLDSWWTSL		12	HBV	env	28	A
IPQYLDSWWTSL		12	HBV	env	28	A
IPQSLYSWWTSL		12	HBV	env	28	A
IPQSLDYWWTSL		12	HBV	env	28	A
IPQSLDSWYTSL		12	HBV	env	28	A
IPQSLDSWWTYL		12	HBV	env	28	A
IPGSLDSWWTSL		12	HBV	env	28	A
IPQSLDSGWTSL		12	HBV	env	28	A
IPQSLDSPWTSL		12	HBV	env	28	A
IPQSLDSWGTSL		12	HBV	env	28	A
IPQSLDSWPTSL		12	HBV	env	28	A
IPQSLDSWWTGL		12	HBV	env	28	A

MURINE CLASS I SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
IPQSLDSWWTPL		12	HBV	env	28	A
IPQVLDSWWTSL		12	HBV	env	28	A
IPQFLDSWWTSL		12	HBV	env	28	A
IPQPLDSWWTSL		12	HBV	env	28	A
IPQMLDSWWTSL		12	HBV	env	28	A
IPQILDSWWTSL		12	HBV	env	28	A
IPQLLDSWWTSL		12	HBV	env	28	A
IPQGLDSWWTSL		12	HBV	env	28	A
IPQTLDSWWTSL		12	HBV	env	28	A
IPQHLDSWWTSL		12	HBV	env	28	A
IPQCLDSWWTSL		12	HBV	env	28	A
IPQNLDSWWTSL		12	HBV	env	28	A
IPQQLDSWWTSL		12	HBV	env	28	A
IPQWLDSWWTSL		12	HBV	env	28	A
IPQDLDSWWTSL		12	HBV	env	28	A
IPQKLDSWWTSL		12	HBV	env	28	A
IPQSLVSWWTSL		12	HBV	env	28	A
IPQSLFSWWTSL		12	HBV	env	28	A
IPQSLPSWWTSL		12	HBV	env	28	A
IPQSLMSWWTSL		12	HBV	env	28	A
IPQSLISWWTSL		12	HBV	env	28	A
IPQSLLSWWTSL		12	HBV	env	28	A
IPQSLGSWWTSL		12	HBV	env	28	A
IPQSLSSWWTSL		12	HBV	env	28	A
IPQSLTSWWTSL		12	HBV	env	28	A
IPQSLHSWWTSL		12	HBV	env	28	A
IPQSLCSWWTSL		12	HBV	env	28	A
IPQSLNSWWTSL		12	HBV	env	28	A
IPQSLQSWWTSL		12	HBV	env	28	A
IPQSLWSWWTSL		12	HBV	env	28	A
IPQSLKSWWTSL		12	HBV	env	28	A
IPSLDSWWTSL		11	HBV	env	28	A
IPQSLDSWTSL		11	HBV	env	28	A
IPQSLDSWWTL		11	HBV	env	28	A
IPQALASWWTSL		12	HBV	env	28	A
IPQSLDSWWTSM		12	HBV	env	28	A
IPQSLDSWWTSF		12	HBV	env	28	A
KTPSFPNI		8	HBV	pol	75	
HAVEFHNL		8	HBV	pol	289	
VSAAFYHL		8	HBV	pol	419	
VIGCYGSL		8	HBV	pol	588	
KQYLNLYPV		9	HBV	pol	668	
CYGSLPQEHI		10	HBV	pol	591	
VSAAFYHL		8	HBV	pol	419	
HAVEFHNL		8	HBV	pol	289	
VIGCYGSL		8	HBV	pol	588	
KTPSFPNI		8	HBV	pol	75	
RPQSLDSWWTSL		12	HBVs	env	28	A

MURINE CLASS I SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
IPQRLDSWWTSL		12	HBVs	env	28	A
IPQSLRSWWTSL		12	HBVs	env	28	A
IPQSLDRWWTSL		12	HBVs	env	28	A
IPQSLDSRWTSL		12	HBVs	env	28	A
IPQSLDSWWRSL		12	HBVs	env	28	A
IPQSLDSWWTRL		12	HBVs	env	28	A
IPQELDSWWTSL		12	HBVs	env	28	A
IPQSLYSWWTSL		12	HBVs	env	28	A
IPQSLDSWETSL		12	HBVs	env	28	A
IPQSLDSWWESL		12	HBVs	env	28	A
VESENKVV		8	HCV	Entire	2253	
AGPYRAFVTI		10	HIV	env	18	A
RAPYRAFVTI		10	HIV	env	18	A
RGPYRAFVTA		10	HIV	env	18	A
KGPYRAFVTI		10	HIV	env	18	A
RGPYRAFVTK		10	HIV	env	18	A
RGPGRAFVTI		10	HIV	env	18	
RGPGRYFVTI		10	HIV	env	18	A
RGPGRAYVTI		10	HIV	env	18	A
RGPGRAFYTI		10	HIV	env	18	A
VESMNKEL		8	HIV	POL	903	
TDSQYALGI		9	HIV	POL	689	
RGAYRAFVTI		10	HIV		18	A
RGPARAFVTI		10	HIV		18	A
RGPYRAAVTI		10	HIV		18	A
RGPYRAFATI		10	HIV		18	A
RGPYRAFVAI		10	HIV		18	A
RGKYRAFVTI		10	HIV		18	A
RGPFRAFVTI		10	HIV		18	A
RGPYKAFVTI		10	HIV		18	A
RGPYRKFVTI		10	HIV		18	A
RGPYRAYVTI		10	HIV		18	A
RGPYRAFKTI		10	HIV		18	A
RGPYRAFVKI		10	HIV		18	A
NEILIRCII		9	HPV	E6	97	
QEKKRHVDL		9	HPV	E6	113	
LFVVYRDSI		9	HPV	E6	52	
FYSRIRELRF		10	HPV	E6	71	A
SSIEFARL		8	HSV		498	
KVPRNQDWL		9	Human	gp100		
VYDFYVWM		8	Human	TRP2		A
KNKFFSYL		8	Human	Tyrosinase	131	
LAVLYCLL		8	Human	Tyrosinase	3	
YMVPFIPL		8	Human	Tyrosinase	425	
GQMNNGSTPM		10	Human	Tyrosinase	157	
IVTMFEAL		8	LCMV	GP	4	
ISHNFCNL		8	LCMV	GP	118	
GVYQFKSV		8	LCMV	GP	70	

MURINE CLASS I SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
HYISMGTSGL		10	LCMV	GP	99	
SGVENPGGYCL		11	LCMV	GP	276	
KAVYNFATM		9	LCMV	GP	33	
CMANNSHHYI		10	LCMV	GP	92	A
CSANNSHHYM		10	LCMV	GP	92	A
SMVENPGGYCL		11	LCMV	GP	276	A
SGVENPGGYCM		11	LCMV	GP	276	A
KAVYNFATM		9	LCMV	GP	33	
KAVYNAATM		9	LCMV	GP	33	A
KAVANFATM		9	LCMV	GP	33	A
KAVYNYATM		9	LCMV	GP	33	A
KAVYNFAAM		9	LCMV	GP	33	A
YTVKYPNL		8	LCMV	NP	205	
FQPQNGQFI		9	LCMV	NP	396	
VGLSYSQTM		9	LCMV	NP	356	
FQPQNGQFI		9	LCMV	NP	396	
FQPQNGQFIHFY		12	LCMV	NP	396	
RPQASGVYM		9	LCMV	NP	118	
RPQASQVYM		9	LCMV	NP	118	A
YTYKYPNL		8	LCMV	NP	205	A
RPQASGVYM		9	LCMV	NP	118	A
RPQASGVAM		9	LCMV	NP	118	A
RPQGSGVYM		9	LCMV	NP	118	A
RPNASGVYM		9	LCMV	NP	118	A
KAVYNFATCGI		11	LCMV			
KAVYNFATB		9	LCMV			
VYAKECTGL		9	Lysteria	listeriolysin	479	
YPHFMPTNL		9	MCMV		168	
YPHYMPTNL		9	MCMV		168	A
HETTYNSI		8	Mouse	beta actin	275	A
YEDTGKTI		8	Mouse	p40 phox RNA	245	
LGYDYSYL		8	Mouse	Tyrosinase	445	
SSMHNALHI		9	Mouse	Tyrosinase	360	
ANFSFRNTL		9	Mouse	Tyrosinase	336	
SYLTLAKHT		9	Mouse	Tyrosinase	136	
HYYVSRDTL		9	Mouse	Tyrosinase	180	
YYVSRDTLL		9	Mouse	Tyrosinase	181	
SFFSSWQII		9	Mouse	Tyrosinase	267	
SYMVPFIPL		9	Mouse	Tyrosinase	424	
PYLEQASRI		9	Mouse	Tyrosinase	466	
SYLTLAKHTI		10	Mouse	Tyrosinase	136	
HYYVSRDTLL		10	Mouse	Tyrosinase	180	
SQVMNLHNL		9	Mouse	TYRP2	363	
YENDIEKKI		9	P. falciparum	CSP	375	
NEEPSDKHI		9	P. falciparum	CSPZ	347	
EEKHEKKHV		9	P. falciparum	LSA1	52	
SYVPSAEQIL		10	P. yoelii	CSP	280	
RYLENGKETL		10	Unknown	HLA-A24	170	

MURINE CLASS I SUPERTYPE						
Sequence	SEQ ID NO.	AA	Organism	Protein	Position	Analog
RYLKNGKETL		10	Unknown	HLA-Cw3	170	
IYTQNRRAL		9	Unknown	P815	12	
VYDFFVWM		8	Unknown	TRP2	181	A
SVYDFFVWL		9	Unknown	TRP2	180	
SVYDFYVWM		9	Unknown	TRP2	180	A
ASNENMDAM		9	unknown			
FAPGYNPAL		9	unknown			
SIQFFGERAL		10	unknown			
SIQFFGEL		8	unknown			
RGYVYQGL		8	VSV	NP	52	
RGPRLNTL		8				
HMWNFIGV		8				
GGAYRLIVF		9				
KYLVTRHADV		19				
FSPRRNGYL		9				
SHYAFSPM		8				
FQPQNGQFI		9				

TABLE 29

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
SGPSNTPPEI		18500	>31000	>10000	8.1		
RNPRFYNL			7.9		>44000		
QPQRGYENF						319	
SEAAYAKKI							3.9
AYAPAKAAI				3.5			
AYAEAKAAI				50			
AYANAKAAI				60			
AYAGAKAAI				48			
AYAVAKAAI				42			
AAAAYAAM			375		>44000		
AAAAYAAAAM			228		>44000		
AAAANAAAM			10960		23		
AAAAAANAAAM			31000		257		
NAIVFKGL			484				
SIINFEKL			3.7				
IFYCPIAI			195				
KVVRFDKL			92				
VYSFSLASRL				303			
SIINFEKL		>37000	1.5	>10000	30508		
KVVRFDKL			37				
SENDRYRLL							13
SFYRNLLWL				>10000	304		
YEANGNLI							0.65
MGLIYNRM			16				
MGYIYNRM			2.3				
MGIIYNRM			14				
MGLIFNRM			21				
MGLIYNRM			9.9				
RMIQNSLTI					4.6		
RLIQNFLTI					40		
GMRQNATEI					81		
YMRVNGKWM					50		
FYIQMATEL				0.31			
FYIQMCTFL				1.1			
AYERMANIL				233			
AYQRMCNIL				2.7			
AYERMCTIL				4.1			
ASNENMETM		>37000	>31000	>10000	33		
TYQRTRALM				69			
TYQKTRALV				44			
TYQPTRALV				17			
TYQFTRALV				371			
TYQLTRALV				110			
SDYEGRLI							0.60
MITQFESL			64				
RTFSFQLI			26				

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
FSVIFDRL			201				
RTFSFQLI			27				
MITQFESL			42				
FSVIFDRL			115				
KSSFYRNL			209				
SSLPFQNI			53				
MNIQFTAV			131				
MNYYWTLL			169				
SFYRNLLWL					46		
SSLPFQNI			9.5				
MNIQFTAV			26				
MNYYWTLL			56				
KSSFYRNL			117				
SIIPSGPL			393				
LSYSAGAL			60				
LSYSAGAL			31				
SSISFCGV			29				
TGICNQNII					13		
ITYKNSTWV					409		
FCGVNSDTV					206		
TGICNQNII					21		
FCGVNSDTV					166		
ITYKNSTWV					276		
SSISFCGV			2.3				
IGRFYIQM			42				
MMIWHSNL			238				
ASNENMETM					41		
IGRFYIQM			24				
MMIWHSNL			287				
FFYRYGFV			350				
KMITQRTI			300				
RSYLIRAL			103				
RFYRTCKL			117				
TALANTIEV					16		
TALANTIEV					3.7		
RSYLIRAL			78				
RFYRTCKL			47				
VYINTALL			65				
VYINTALL			14				
VYIEVLHL			75				
VYIEVLHL			21				
WYIPPSLRTL				96			
MURTAZAKDPE PTIDES				0.96			
IYSTVASSL				4.1			
LYEKVKSQL				2.2			
LYQKVKSQL				2.8			
LYEKMKSQL				1.6			

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
LYEKVFSQL				7.4			
LYQNVGTYV				6.9			
MGLKFRQL			7.4				
VSYVNTNM			60				
SYVNTNMGL				19			
MGLKFRQL			6.3				
VSYVNTNM			33				
SYVNTNMGL				12			
WGPSLYSI		17					
ASARFSWL			323				
WGPSLYSIL		6.6					
TGPCRTCMT		108					
WYWGPSLYSI				8.3			
IPQSLDSWWTSL						2.2	
IPQSLDSYWTSL						2.7	
ASARFSWL			49				
WYWGPSLYSI				16			
APQSLDSWWTSL						15	
IPQALDSWWTSL						6.1	
IPQSLASWWTSL						4.2	
IPQSLDAWWTSL						4.0	
IPQSLDSAWTSL						13	
IPQSLDSWWASL						0.34	
IPQSLDSWWTAL						134	
EPQSLDSWWTSL						86	
IPESLDSWWTSL						13	
IPQSLDEWWTSL						1.9	
IPQSLDSWWTEL						3.0	
RPQSLDSWWTSL						60	
IPRSLDSWWTSL						160	
IPQRLDSWWTSL						23	
IPQSRDSWWTSL						21	
IPQSLRSWWTSL						12	
IPQSLDRWWTSL						5.0	
IPQSLDSRWTSL						47	
IPQSLDSWWRSL						485	
IPQSLDSWWTRL						196	
YPQSLDSWWTSL						91	

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
IPYSLDSWWTSL						0.78	
IPQYLDSWWTSL						92	
IPQSLYSWWTSL						4.7	
IPQSLDYWWTSL						1.6	
IPQSLDSWYTSL						17	
IPQSLDSWWTYL						0.89	
IPGSLDSWWTSL						24	
IPQSLDSGWTSL						70	
IPQSLDSPWTSL						19	
IPQSLDSWGTSL						138	
IPQSLDSWPTSL						60	
IPQSLDSWWTGL						2.5	
IPQSLDSWWTPL						1.2	
IPQVLDSWWTSL						5.1	
IPQFLDSWWTSL						4.3	
IPQPLDSWWTSL						6.3	
IPQMLDSWWTSL						4.1	
IPQILDSWWTSL						12	
IPQLLDSWWTSL						0.25	
IPQGLDSWWTSL						2.7	
IPQTLDSWWTSL						7.7	
IPQHLDSWWTSL						39	
IPQCLDSWWTSL						25	
IPQNLDSWWTSL						12	
IPQQLDSWWTSL						1.7	
IPQWLDSWWTSL						3.7	
IPQDLDSWWTSL						22	
IPQKLDSWWTSL						9.3	
IPQSLVSWWTSL						11	
IPQSLFSWWTSL						11	
IPQSLPSWWTSL						16	
IPQSLMSWWTSL						0.95	
IPQSLISWWTSL						17	
IPQSLLSWWTSL						0.84	
IPQSLGSWWTS						2.7	

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
IPQSLSSWWTSL						0.49	
IPQSLTSWWTSL						1.7	
IPQSLHSWWTSL						1.5	
IPQSLCSWWTSL						1.1	
IPQSLNSWWTSL						1.5	
IPQSLQSWWTSL						0.81	
IPQSLWSWWTSL						2.4	
IPQSLKSWWTSL						1.1	
IPSLDSWWTSL						119	
IPQSLDSWTSL						0.22	
IPQSLDSWWTL						1.3	
IPQALASWWTSL						26	
IPQSLDSWWTSM						0.80	
IPQSLDSWWTSF						1.9	
KTPSFPNI			270				
HAVEFHNL			49				
VSAAFYHL			7.0				
VIGCYGSL			157				
KQYLNLYPV					3.4		
CYGSLPQEHI				303			
VSAAFYHL			5.2				
HAVEFHNL			158				
VIGCYGSL			63				
KTPSFPNI			155				
RPQSLDSWWTSL						144	
IPQRLDSWWTSL						34	
IPQSLRSWWTSL						11	
IPQSLDRWWTSL						2.0	
IPQSLDSRWTSL						2.6	
IPQSLDSWWRSL						335	
IPQSLDSWWTRL						27	
IPQELDSWWTSL						18	
IPQSLYSWWTSL						8.3	
IPQSLDSWETSL						5.3	
IPQSLDSWWESL						394	
VESENKVV							349
AGPYRAFVTI		5.0					

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
RAPYRAFVTI		176					
RGPYRAFVTA		126					
KGPYRAFVTI		5.8					
RGPYRAFVTK		91					
RGPGRAFVTI		9.7	31000	>10000	22000		
RGPGRYFVTI		2.7					
RGPGRAYVTI		14					
RGPGRAFYTI		7.2					
VESMNKEL							114
TDSQYALGI							179
RGAYRAFVTI		3.4					
RGPARAFVTI		1.04					
RGPYRAAVTI		2.0					
RGPYRAFATI		2.1					
RGPYRAFVAI		1.3					
RGKYRAFVTI		67					
RGPFRAFVTI		0.78					
RGPYKAFVTI		13					
RGPYRKFVTI		3.6					
RGPYRAYVTI		2.1					
RGPYRAFKTI		2.3					
RGPYRAFVKI		3.9					
NEILIRCII							12
QEKKRHVDL							256
LFVVYRDSI				453			
FYSRIRELRF				447			
SSIEFARL			1.8	>10000			
KVPRNQDWL					38		
VYDFYVWM			145				
KNKFFSYL			57				
LAVLYCLL			72				
YMVPFIPL			70				
GQMNNGSTPM					242		
IVTMFEAL			82				
ISHNFCNL			411				
GVYQFKSV			11				
HYISMGTSGL				83			
SGVENPGGYCL			>31000		60		
KAVYNFATM					3.3		
CMANNSHHYI					220		
CSANNSHHYM					42		
SMVENPGGYCL					154		
SGVENPGGYCM					128		
KAVYNFATM					1.5	>27000	
KAVYNAATM					2.0	>27000	
KAVANFATM					1.2	27000	
KAVYNYATM					2.1	>27000	
KAVYNFAAM					4.4	27000	

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
YTVKYPNL			204				
FQPQNGQFI					6.9		
VGLSYSQTM			71				
FQPQNGQFI			>31000		4.9		
FQPQNGQFIHFY			15500		280		
RPQASGVYM			>31000		>44000	0.99	
RPQASQVYM						3.8	
YTYKYPNL			1.8				
RPQASGVYM						3.0	
RPQASGVAM						12	
RPQGSGVYM						39	
RPNASGVYM						19	
KAVYNFATCGI					29		
KAVYNFATB					7.9		
VYAKECTGL				129			
YPHFMPTNL						7.5	
YPHYMPTNL						9.5	
HETTYNSI							1.8
YEDTGKTI							0.86
LGYDYSYL			3.4				
SSMHNALHI					7.6		
ANFSFRNTL			6.0				
SYLTLAKHT				188			
HYYVSRDTL				43			
YYVSRDTLL				99			
SFFSSWQII				16			
SYMVPFIPL				144			
PYLEQASRI				173			
SYLTLAKHTI				4.4			
HYYVSRDTLL				167			
SQVMNLHNL					2.3		
YENDIEKKI							3.8
NEEPSDKHI							40
EEKHEKKHV							284
SYVPSAEQIL				280			
RYLENGKETL				80			
RYLKNGKETL				217			
IYTQNRRAL				144			
VYDFFVWM			464				
SVYDFFVWL			1.0				
SVYDFYVWM			1.2		3365		
ASNENMDAM					28		
FAPGYNPAL			2.0				
SIQFFGERAL			21		>44000		
SIQFFGEL			16		>44000		
RGYVYQGL		>37000	2.1	>10000	>44000		
RGPRLNTL		186					
HMWNFIGV			202				

MURINE CLASS I SUPERTYPE							
Sequence	SEQ ID NO.	Dd	Kb	Kd	Db	Ld	Kk
GGAYRLIVF		3.5					
KYLVTRHADV				33			
FSPRRNGYL		2.7					
SHYAFSPM			250		>88000		
FQPQNGQFI			9513		17		